

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
  
OM protein - protein search, using sw model  
Run on: February 4, 2006, 18:08:56 ; Search time 46 Seconds  
(without alignments)  
1169.243 Million cell updates/sec

Title: US-10-633-835-2  
Perfect score: 2907  
Sequence: 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDLTAERPPADLAV 559

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2896	99.6	2185	1 S60200	acetyl-CoA carboxy
2	2190	75.3	2288	2 T30568	acetyl-CoA carboxy
3	2090.5	71.9	2280	2 T38906	acetyl-CoA carboxy
4	2060	70.9	2233	2 S63347	acetyl-CoA carboxy
5	2060	70.9	2279	2 T42531	acetyl-CoA carboxy
6	1785	61.4	2345	1 A35578	acetyl-CoA carboxy
7	1782	61.3	2339	2 S41121	acetyl-CoA carboxy
8	1781	61.3	2346	2 I38928	acetyl-CoA carboxy
9	1780	61.2	2324	1 A29924	acetyl-CoA carboxy
10	1754.5	60.4	2123	2 S55089	probable acetyl-Co
11	1598.5	55.0	640	2 T07923	acetyl-CoA carboxy
12	1583	54.5	2304	2 T07920	probable acetyl-Co
13	1581.5	54.4	2359	2 E86483	probable acetyl-Co
14	1579	54.3	2257	2 D86483	protein F5U5.19 [i
15	1577.5	54.3	2257	2 T09538	acetyl-CoA carboxy
16	1569.5	54.0	2311	2 T06161	acetyl-CoA carboxy
17	1565	53.8	2257	1 A57710	acetyl-CoA carboxy
18	1558.5	53.6	2261	2 T07084	acetyl-CoA carboxy
19	1555.5	53.5	1978	2 T07081	acetyl-CoA carboxy
20	1543.5	53.1	2325	2 T02235	acetyl-CoA carboxy
21	1502.5	51.7	2089	1 A48757	acetyl-CoA carboxy
22	1314	45.2	2054	2 T32413	probable acetyl-Co
23	1121	38.6	1657	2 T25421	hypothetical prote
24	769	26.5	371	2 T07938	probable acetyl-Co
25	724	24.9	491	2 A69123	biotin carboxylase
26	709.5	24.4	447	2 AH1923	biotin carboxylase
27	709.5	24.4	447	2 A53311	biotin carboxylase
28	679	23.4	453	2 H81978	probable acetyl-Co
29	676	23.3	450	2 A69581	acetyl-CoA carboxy

30	675	23.2	506	2 D69277	biotin carboxylase
31	671.5	23.1	448	2 S74380	biotin carboxylase
32	668	23.0	455	2 G71860	biotin carboxylase
33	667	22.9	453	2 F81033	acetyl-CoA carboxy
34	666	22.9	662	2 G95929	probable methylcro
35	662	22.8	458	2 B64566	biotin carboxylase
36	660.5	22.7	667	2 AB3352	propionyl-CoA carb
37	660	22.7	452	2 C83998	acetyl-CoA carboxy
38	658.5	22.7	445	2 B75558	acetyl-CoA carboxy
39	656.5	22.6	667	2 F98286	hypothetical prote
40	656.5	22.6	677	2 AC2997	hypothetical prote
41	655.5	22.5	455	2 B86722	biotin carboxylase
42	653.5	22.5	448	2 G87482	acetyl-CoA carboxy
43	649	22.3	501	2 D64453	biotin carboxylase
44	645	22.2	449	1 JS0632	acetyl-CoA carboxy
45	642	22.1	449	2 H91144	hypothetical prote

ALIGNMENTS

RESULT 1  
S60200  
acetyl-CoA carboxylase (EC 6.4.1.2) - smut fungus (Ustilago maydis)  
C/Species: Ustilago maydis (corn smut)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: S60200; S49991  
R/Bailey, A.; Keon, J.; Owen, J.; Hargreaves, J.  
Mol. Gen. Genet. 249, 191-201, 1995  
A/Title: The ACC1 gene, encoding acetyl-CoA carboxylase, is essential for growth in Ustilago maydis  
A/Reference number: S60200; MUID:96086936; PMID:7500941  
A/Accession: S60200  
A/Molecule type: DNA  
A/Residues: 1-2185 <BAI>  
A/Cross-references: UNIPROT:Q12721; UNIPARC:UPI000006A8BA; EMBL:Z46886; NID:9600097; P:9600097  
C/Genetics: ACC1  
A/Gene: ACC1  
A/Introns: 14/1  
C/Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin carboxylase homology; lipoyl/biotin binding; ligase  
C/Keywords: biotin binding; ligase  
F/41-548/Domain: biotin carboxylase homology <BCH>  
F/675-747/Domain: lipoyl/biotin-binding homology <LPB>  
F/714/Binding site: biotin (Lys) (covalent) #status predicted

Query Match	99.6%;	Score	2896;	DB 1;	Length	2185;																																																						
Best Local Similarity	99.6%;	Pred. No.	1.9e-197;																																																									
Matches	557;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;																																																			
QY	1	PPPDHKA	V	SQ	F	I	G	N	P	L	E	T	A	P	S	P	V	A	D	F	I	R	K	Q	G	H	S	V	I	T	K	V	L	I	C	N	G	I	A	A	V	K	E	I	R	S	I	R	K	W	60									
Db	2	PPPDHKA	V	SQ	F	I	G	N	P	L	E	T	A	P	S	P	V	A	D	F	I	R	K	Q	G	H	S	V	I	T	K	V	L	I	C	N	G	I	A	A	V	K	E	I	R	S	I	R	K	W	61									
QY	61	AYETFG	D	E	R	A	I	E	F	T	M	A	T	P	E	D	L	K	V	N	A	D	Y	I	R	M	A	D	Q	Y	V	E	V	P	G	S	N	N	N	N	Y	A	N	V	D	L	I	V	D	V	A	E	R	A	120					
Db	62	AYETFG	D	E	R	A	I	E	F	T	M	A	T	P	E	D	L	K	V	N	A	D	Y	I	R	M	A	D	Q	Y	V	E	V	P	G	S	N	N	N	N	Y	A	N	V	D	L	I	V	D	V	A	E	R	A	121					
QY	121	GVHAVW	A	G	W	G	H	A	S	E	N	P	R	L	P	E	S	L	A	S	K	H	K	I	I	F	I	G	P	P	G	S	A	M	R	S	L	G	D	K	I	S	S	T	I	V	A	Q	H	A	D	V	P	C	M	180				
Db	122	GVHAVW	A	G	W	G	H	A	S	E	N	P	R	L	P	E	S	L	A	S	K	H	K	I	I	F	I	G	P	P	G	S	A	M	R	S	L	G	D	K	I	S	S	T	I	V	A	Q	H	A	D	V	P	C	M	181				
QY	181	PW	S	G	T	G	I	K	E	T	M	S	D	Q	G	F	L	T	V	S	D	D	V	Y	Q	A	C	I	H	T	A	E	E	G	L	E	K	A	E	K	I	G	Y	P	V	M	I	K	A	S	E	G	G	G	K	G	I	240		
Db	182	PW	S	G	T	G	I	K	E	T	M	S	D	Q	G	F	L	T	V	S	D	D	V	Y	Q	A	C	I	H	T	A	E	E	G	L	E	K	A	E	K	I	G	Y	P	V	M	I	K	A	S	E	G	G	G	K	G	I	241		
QY	241	RK	C	T	N	G	E	E	F	K	Q	L	Y	N	A	V	L	G	E	V	P	G	S	P	V	F	V	M	K	L	A	Q	A	R	H	L	E	V	Q	L	L	A	D	Q	Y	G	N	A	I	S	I	F	G	R	D	C	S	V	Q	300
Db	242	RK	C	T	N	G	E	E	F	K	Q	L	Y	N	A	V	L	G	E	V	P	G	S	P	V	F	V	M	K	L	A	Q	A	R	H	L	E	V	Q	L	L	A	D	Q	Y	G	N	A	I	S	I	F	G	R	D	C	S	V	Q	301
QY	301	RR	H	Q	K	I	E	E	A	P	V	T	I	A	P	E	D	A	R	E	S	M	E	K	A	A	V	R	L	A	K	L	V	G	Y	S	A	G	T	V	E	W	L	Y	S	P	E	S	G	E	F	A	F	L	E	I	N	P	360	
Db	302	RR	H	Q	K	I	E	E	A	P	V	T	I	A	P	E	D	A	R	E	S	M	E	K	A	A	V	R	L	A	K	L	V	G	Y	S	A	G	T	V	E	W	L	Y	S	P	E	S	G	E	F	A	F	L	E	I	N	P	361	
QY	361	RL	Q	V	E	H	P	T	T	E	M	V	S	G	V	N	I	P	A	A	Q	L	V	A	M	G	I	P	L	Y	S	I	R	D	I	R	T	L	Y	G	M	D	P	R	G	N	E	I	D	F	D	F	S	S	P	E	S	F	420	

Db 362 RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESF 421

Qy 421 KTQRKPQPGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480

Db 422 KTQRKPQPGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVAASGALHEYA 481

Qy 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 540

Db 482 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 541

Qy 541 DGLIQDRLTAERPPADLAV 559

Db 542 DGLIQDRLTAERPPADLAV 560

RESULT 2

T30568

acetyl-CoA carboxylase (EC 6.4.1.2) - Emericella nidulans

C;Species: Emericella nidulans, Aspergillus nidulans

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T30568

R;Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.

Curr. Genet. 34, 379-385, 1998

A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergil

A;Reference number: Z20869; MUID:99087906; PMID:9871120

A;Accession: T30568

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2288 <MOR>

A;Cross-references: UNIPROT:O60033; UNIPARC:UPI000006C49E; EMBL:Y15996; NID:G3021302; PT

C;Genetics:

A;Gene: accA

A;Introns: 54/3; 111/3

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

C;Keywords: ligase

Query Match 75.3%; Score 2190; DB 2; Length 2288;

Best Local Similarity 74.8%; Pred. No. 3.8e-147;

Matches 415; Conservative 53; Mismatches 87; Indels 0; Gaps 0;

Qy 5 HKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAVKEIRSKWAYET 64

Db 19 HNLPSHFIGNHLDAAPSSVKDFVANHEGHSVITSVLIANNGIAAVKEIRSVRKWAYET 78

Qy 65 FGDERAIEFTVMATPEDLKNADYIRMADQYVEVPGGSSNNNNYANVDLIVDVAERAGVHA 124

Db 79 FGNERAIQFTVMATPEDLANADYIRMADQYVEVPGGTNNNNYANVELIVDVAERMDVHA 138

Qy 125 VWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSG 184

Db 139 VWAGWGHASENPRLPESLAASKHKIIFIGPPASAMRSLGDKISSTIVAQAHAQVPCIPWSG 198

Qy 185 TGIKETMMSDQGFLTVDVDDVYQQACIHTAEEGLEKAEKIGYPMVMIKASEGGGKGIRKCT 244

Db 199 TGDEVKVDENGIVTVEEVEVNGKCTFSPEEGLEKAKQIGPPVMIKASEGGGKGIRKVE 258

Qy 245 NGEFEKQLYNAVLEVPVGMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQ 304

Db 259 KEEDFINLYNAAANEIPGSPIFIMKLAGNARHLEVQLLADQYGNNISLFGDCSVQRRHQ 318

Qy 305 KIIEAPVTIAPEDARESMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364

Db 319 KIIEAPVTIANPTTFQAMERAAVSLGKLGVYSAGTVEYLYSHADDKFYFLELNPRLQV 378

Qy 365 EHPTTEMVSGVNIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESFQTR 424

Db 379 EHPTTEMVTGNLPAALQIAMGIFLHRIRDIRLLYGVDPNTSAEIDFDFSSEESFQTR 438

Qy 425 KPQPGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484

Db 439 RPQPKGHTTACRITSEDPGEGFKPSSGTMHELNFRSSNVMGYFSVGTAGGHSFSDSQF 498

Qy 485 GHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLDGLI 544

Db 499 GHIFAYGENFSASRKHVMIALKELSIRGDFRTTIEYLIKLETPAFENKITTGWLDQLI 558

Qy 545 QDRLTAERPPADLAV 559

Db 559 SNKLTARPDTTIAV 573

RESULT 3

T38906

acetyl-CoA carboxylase (EC 6.4.1.2) [similarity] - fission yeast (Schizosaccharomyces f

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T38906

R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21813

A;Accession: T38906

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2280 <CON>

A;Cross-references: UNIPROT:P78820; UNIPARC:UPI0000127CAE; EMBL:Z99261; PIDN:CAB16395.1

A;Experimental source: strain 972h-; cosmid c56E4

C;Genetics:

A;Gene: SPDB:SPAC56E4.04c

A;Map position: 1

A;Introns: 44/1

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin

C;Keywords: ligase

Query Match 71.9%; Score 2090.5; DB 2; Length 2280;

Best Local Similarity 71.4%; Pred. No. 4.6e-140;

Matches 396; Conservative 62; Mismatches 96; Indels 1; Gaps 1;

Qy 6 KAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAVKEIRSKWAYETF 65

Db 37 RVASHFLGGSLDKAPAGKVXDYIASHGGHTVITSILIANNGIAAVKEIRSKWAYETF 96

Qy 66 GDERAIEFTVMATPEDLKNADYIRMADQYVEVPGGSSNNNNYANVDLIVDVAERAGVHAV 125

Db 97 NNERAIKFTVMATPDDLKNADYIRMADQYVEVPGGSSNNNNYANVELIVDIAERMNVHAV 156

Qy 126 WAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGT 185

Db 157 WAGWGHASENPKLPEMLSSASSKKIVFIGPPGSAMRSLGDKISSTIVAQSAARVPCMSWSGN 216

Qy 186 GIKETMMSDQ-CFLTVDVDDVYQQACIHTAEEGLEKAEKIGYPMVMIKASEGGGKGIRKCT 244

Db 217 ELDOVRIDEETNIVTDDVYQKACIRSAEGIAVAEKIGYPMVMIKASEGGGKGIRQVT 276

Qy 245 NGEFEKQLYNAVLEVPVGMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQ 304

Db 277 STEKFAQAFQOVLDELPGSPVFMKLAGQARHLEVQILADQYGNNISLFGDCSVQRRHQ 336

Qy 305 KIIEAPVTIAPEDARESMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364

Db 337 KIIEAPVTIAPATFHEMERAARLGLVGYASAGTIEYLYEPENDRFYFLELNPRLQV 396

Qy 365 EHPTTEMVSGVNIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESFQTR 424

Db 397 EHPTTEMVSGVNLPAALQVAMGLPLSRIPHIRELYGLPRDGDSEIDFFQNPESFKVQK 456

Qy 425 KPQPGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484

Db 457 VPTPKGHCVACKITSEDPGEGFKPSSGMIKDLNFRSSNVMGYFSVGTAGGHEFADSQF 516

Qy 485 GHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLDGLI 544

Db 517 GHIFSFAESRESSRKSMMVVALKELSIRGDFRTTVEYLVRLLETKEFSENEFTTGWLDRLI 576

Qy 545 QDRLTAERPPADLAV 559

Db 577 AQVTSARPDKMLAV 591

RESULT 4

S63347

acetyl-CoA carboxylase (EC 6.4.1.2) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein N3175; protein YNR016c

C:Species: Saccharomyces cerevisiae

C:Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004

C:Accession: S63347; S31249

R:Pohl, T.M.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63346

A:Accession: S63347

A:Molecule type: DNA

A:Residues: 1-2233 <POH>

A:Cross-references: UNIPROT:Q00955; UNIPARC:UPI0000127CAF; EMBL:Z71631; NID:g1302497; PI

A:Experimental source: strain S288C

R:Al-Feel, W.; Chirala, S.S.; Wakil, S.J.

Proc. Natl. Acad. Sci. U.S.A. 89, 4534-4538, 1992

A:Title: Cloning of the yeast FAS3 gene and primary structure of yeast acetyl-CoA carbox

A:Reference number: S31249; MUID:92262474; PMID:1350093

A:Accession: S31249

A:Molecule type: DNA

A:Residues: 1-1522, 'G', 1524-1755, 'WYRCL', 1756-1760, 'ESTN', 1761, 1767-2233 <ALF>

A:Cross-references: UNIPARC:UPI0000145F95; EMBL:M92156; NID:g402313; PIDN:AAA20073.1; PI

C:Genetics:

A:Gene: SGD:ACC1; FAS3; ABP2

A:Cross-references: SGD:S0005299; MIPS:YNR016c

A:Map position: 14R

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

C:Keywords: biotin binding; fatty acid biosynthesis; ligase

F:61-569/Domain: biotin carboxylase homology <BCH>

F:696-768/Domain: lipoyl/biotin-binding homology <LPB>

F:735/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 70.9%; Score 2060; DB 2; Length 2233;

Best Local Similarity 69.1%; Pred. No. 6.6e-138;

Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;

QY 3 PDHKAVSQFTGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAA VKEIRSIRKWAY 62

Db 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAA VKEIRSIRKWAY 83

QY 63 ETFGDERATEFTVMATPEDLKVNDYIRMDQYVEVPGGSSNNNNYANVDLIVDVAERAGV 122

Db 84 ETFGDDRTVQFVAMATPEDLEANA EYIRMDQYIEVPGGTNNNNYANVDLIVDIAERADV 143

QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKTSSTIVAQHADVPCMPW 182

Db 144 DAVWAGWGHASENPLLPKLSQSKRVIFIGPPGNAMRSLGDKISSTIVAQSAKVPCIPW 203

QY 183 SGTGKETMMSDQ--GFLTVDVYQQACIHTAEGLEKAEKIGYPMVMIKASEGGGKGKI 240

Db 204 SGTGV-DTVHVEKTGLSVSDDDIYQKGCCTSPEDGLQKAKRIGFFPMVMIKASEGGGKGKI 262

QY 241 RKCTNGEEFKQLYNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300

Db 263 RQVEREEDFIALYHOANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGSDCSVQ 322

QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360

Db 323 RRHQKIIIEAPVTIAKAETTHEMEKAAVRLGKLVGYVSAGTVELYSHDDGKFYFLELNP 382

QY 361 RLQVEHPTEMVSGWNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPESF 420

Db 383 RLQVEHPTEMVSGWNLPAALQLIAMGIPMHRISDITLYGMNPHSAEIDFEFTQDAT 442

QY 421 KTQRKPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGVSFVSGTSGALHEYA 480

Db 443 KKQRRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGVSFVSGNNGNIHFS 502

QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAPESNKITTTGWL 540

Db 503 DSQFGHIFAPGENRQASRKHMVVALKELSI RGDFTTVEYLIKLETFEDFDNTITTTGWL 562

QY 541 DGLIQDRLTAERPPADLAV 559

Db 563 DDLITHKMTAEKPDPTLAV 581

RESULT 5

T42531

acetyl-CoA carboxylase (EC 6.4.1.2) - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: acetyl-coenzyme A carboxylase

C:Species: Schizosaccharomyces pombe

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2002

C:Accession: T42531

R:Saito, A.; Kazuta, Y.; Toh, H.; Kondo, H.; Tanabe, T.

submitted to the EMBL Data Library, October 1997

A:Description: Biotin-dependent enzymes in Schizosaccharomyces pombe: cloning and nucl

A:Reference number: Z22171

A:Accession: T42531

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2279 <SAI>

A:Cross-references: UNIPARC:UPI00001690FB; EMBL:D78169; PIDN:BAA11238.1

A:Experimental source: strain HM123

C:Genetics:

A:Introns: 44/1

C:Function:

A:Description: catalyzes the carboxylation of acetyl-CoA to malonyl-CoA using carboxyl

A:Pathway: fatty acid biosynthesis

A>Note: committed step of fatty acid biosynthesis

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti

C:Keywords: biotin metabolism; fatty acid biosynthesis; ligase

Query Match 70.9%; Score 2060; DB 2; Length 2279;

Best Local Similarity 70.6%; Pred. No. 6.8e-138;

Matches 392; Conservative 64; Mismatches 97; Indels 2; Gaps 2;

QY 6 KAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAA VKEIRSIRKWAYETF 65

Db 37 RVASHPLGNSLDKAPAGKVVDYIASHGGHTVITSILLIANNNGIAA VKEIRSIRKWAYETF 96

QY 66 GDERAIEFTVMATPEDLKVNDYIRMDQYVEVPGGSSNNNNYANVDLIVDVAERAGVHAV 125

Db 97 NNERAIKFTVMATPDDLKVNDYIRMDQYVEVPGGSSNNNNYANVELIVDIAERMNVHAV 156

QY 126 WAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT 185

Db 157 WAGWGHASENPKLPEMLSASSKKIVIFIGPPGSAMRSLGDKISSTIVAQ SARVPCMSWSGN 216

QY 186 GIKETMMSDQ-GFLTVDVYQQACIHTAEGLEKAEKIGYPMVMIKASEGGGKGIRKCT 244

Db 217 ELDQVRIDEETNIVTDDVYQKACIRSAEAGIAVEKIGYSVMIKASEGGGKGIRQVT 276

QY 245 NGEEFKQLYNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQ 304

Db 277 STEKFAQAFQOVLDELPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQ 336

QY 305 KIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364

Db 337 KIL-EAPVTIAPATTHEMERAARVLGELVGYASAGTIEYLYEPENDRIFYLELNPRLQV 395

QY 365 EHPTTEMVSGWNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPESFKTOR 424

Db 396 EHPTTEMVSGWNLPAALQVAMGLPLSRIPHIRELYGLPRDGDSEIDFFQNPESFKVQK 455

QY 425 KPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGVSFVSGTSGALHEYADSOF 484

Db 456 VPTPKGHCVACRITSEDPGEGFKPSSGMIXKOLNFRSSSNVWGVSFVSGTAGIHEFSDSOF 515

QY 485 GHIPAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAPESNKITTTGWL DGLI 544

Db 516 GHIFSPSTESRESSRKSMMVVALKELSI RGDFTTVEYILVRLLETKEFSENEFTTTGWLDRLI 575



Qy 545 QDRLTAERPPADLAV 559  
: : : : :  
Db 576 AQKVTSAEPDKMLAV 590  
:  
RESULT 6  
A35578  
acetyl-CoA carboxylase (EC 6.4.1.2) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004  
C:Accession: A35578; A37119; I59145; I70069; I70070; I55305  
R:Lopez-Casillas, F.; Bai, D.H.; Luo, X.; Kong, I.S.; Hermodson, M.A.; Kim, K.H.  
Proc. Natl. Acad. Sci. U.S.A. 85, 5784-5788, 1988  
A:Title: Structure of the coding sequence and primary amino acid sequence of acetyl-coen  
A:Reference number: A35578; MUID:88320328; PMID:2901088  
A:Accession: A35578  
A:Molecule type: mRNA  
A:Residues: 1-2345 <LOP>  
A:Cross-references: UNIPROT:P11497; UNIPARC:UPI0000127C7B; GB:J03808; NID:G202644; PIDN:  
R;Kong, I.S.; Lopez-Casillas, F.; Kim, K.H.  
J. Biol. Chem. 265, 13695-13701, 1990  
A:Title: Acetyl-CoA carboxylase mRNA species with or without inhibitory coding sequence  
A:Reference number: A37119; MUID:90337981; PMID:1974251  
A:Accession: A37119  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1167-1200 <KON>  
A:Cross-references: UNIPARC:UPI000017312F; GB:M55315  
A:Experimental source: clone lambdaDHN121  
R;Luo, X.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4042-4046, 1989  
A:Title: Structural features of the acetyl-CoA carboxylase gene: Mechanism for the gener  
A:Reference number: I59145; MUID:89264558; PMID:2566999  
A:Accession: I59145  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-74 <RES>  
A:Cross-references: UNIPARC:UPI0000170BB7; GB:M26731; NID:G202641; PIDN:AAA40652.1; PID:  
A:Experimental source: hepatic  
R:Lopez-Casillas, F.; Kim, K.  
J. Biol. Chem. 264, 7176-7184, 1989  
A:Title: Heterogeneity at the 5' end of rat acetyl-coenzyme A carboxylase mRNA: Lipogeni  
A:Reference number: I55305; MUID:89214151; PMID:2565337  
A:Accession: I70069  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-33 <RE2>  
A:Cross-references: UNIPARC:UPI000017084D; GB:M26196; NID:G202649; PIDN:AAA40655.1; PID:  
A:Accession: I70070  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-33 <RE3>  
A:Cross-references: UNIPARC:UPI000017084D; GB:M26197; NID:G202651; PIDN:AAA40656.1; PID:  
A:Accession: I55305  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-33 <RE4>  
A:Cross-references: UNIPARC:UPI000017084D; GB:M26195; NID:G202647; PIDN:AAA40654.1; PID:  
A:Experimental source: hepatic  
C:Comment: This enzyme catalyzes the carboxylation of acetyl CoA to malonyl CoA and is t  
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-  
C:Keywords: biotin binding; ligase  
F;119-619/Domain: biotin carboxylase homology <BCH>  
F;746-818/Domain: lipoyl/biotin-binding homology <LPB>  
F;785/Binding site: biotin (Lys) (covalent) #status predicted

Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
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Query Match 61.4%; Score 1785; DB 1; Length 2345;  
Best Local Similarity 63.6%; Pred. No. 2.7e-118;  
Matches 344; Conservative 80; Mismatches 103; Indels 14; Gaps 5;

Db 102 ASP-AEFVTRFGGNKVIKVLIANNGIAAACKMRISRRWSYEMFRNERAIRFVVMVTPED 160  
:  
Qy 82 LKVNADYIRMAADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHAASENRLPES 141  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 161 LKANAHEYIKMADHYVPVPGGANNNNYANVELILDIAKRIPIVQAVWAGWGHAASENKLPEL 220  
:  
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGSGTGKIKETMMSD---QGFL 198  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 221 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGITPLPWSGSLRVDWQENDEFSKRIL 278  
:  
Qy 199 TVSDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLG 258  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 279 NVFPQDLYEKGYYKVDVDDGLKAAEEVGYPMIKASEGGGKGIRKVNADDFPNLFQVQA 338  
:  
Qy 259 EYVGPSPFVMKLAGQARHLEVLQADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPED 318  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 339 EVFGSPIFVMRLAKQSRHLEVLQADQYGNASISLFGDCSVQRRHQKIIIEEAPAAIATPA 398  
:  
Qy 319 ARESMEKAAVRLAKLVGYVSAGTVWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP 378  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 399 VFEHMEQCAVKLAKWGYVSAGTVWLYS-QDGSFYFLELNPRLOVEHPTTEMVADVNL 457  
:  
Qy 379 AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFSSPESFKTQRKPOQGHVVACRIT 438  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 458 AAQLQIAMGIPLFRIKDIRMYGVSPWGDAPIDFENSA-----HVPCPRGHVIAARIT 510  
:  
Qy 439 AENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEAR 498  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 511 SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGLHFEFADSFQGHCFSGWGENREAI 570  
:  
Qy 499 KQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLGLIQDRLTAERPPADLA 558  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 571 SNMVVALKELSIRGDFRTTVEYLIKLLETSFQLNRIDITGWLDRLIAEKVQAERPDITMLG 630  
:  
Qy 559 V 559  
|  
Db 631 V 631  
:  
RESULT 7  
S41121  
acetyl-CoA carboxylase (EC 6.4.1.2) - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 11-Jan-2002  
C:Accession: S41121  
R;Ha, J.; Daniel, S.; Kong, I.S.; Park, C.K.; Tae, H.J.; Kim, K.H.  
Eur. J. Biochem. 219, 297-306, 1994  
A:Title: Cloning of human acetyl-CoA carboxylase cDNA.  
A:Reference number: S41121; MUID:94139704; PMID:7905825  
A:Accession: S41121  
A:Molecule type: mRNA  
A:Residues: 1-2339 <HAJ>  
A:Cross-references: UNIPARC:UPI000011EDF5; EMBL:X68968; NID:G452315; PIDN:CAA48770.1; I  
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin  
C:Keywords: biotin binding; ligase  
F;120-620/Domain: biotin carboxylase homology <BCH>  
F;747-819/Domain: lipoyl/biotin-binding homology <LPB>  
F;786/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 61.3%; Score 1782; DB 2; Length 2339;  
Best Local Similarity 63.6%; Pred. No. 4.4e-118;  
Matches 344; Conservative 78; Mismatches 105; Indels 14; Gaps 5;

Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 103 ASP-ABFVTRFGGNKVIKVLIANNGIAAACKMRISRRWSYEMFRNERAIRFVVMVTPED 161  
:  
Qy 82 LKVNADYIRMAADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHAASENRLPES 141  
||| |:| : ||| ||||| :|||:| :||| | |||  
Db 162 LKANAHEYIKMADHYVPVPGGANNNNYANVELILDIAKRIPIVQAVWAGWGHAASENKLPEL 221  
:  
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGSGTGKIKETMMSD---QGFL 198  
||| |:| : ||| ||||| :|||:| :||| | |||



Db 222 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSLRVDMQENDFSKRIL 279  
Qy 199 TVSDVVYQACIHTAEEGLEKAEGKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258  
Db 280 NVPQELYEGYVKDVGDLQAEEVGYPMIKASEGGGKGIRKVNADDFPNLFRQVQA 339  
Qy 259 EVPGPSVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEAPVTIAPED 318  
Db 340 EVPGPSIFVMRLAKQSRHLEVQILADQYGNNAISLFGDCSVQRRHQKIIIEAPATIATPA 399  
Qy 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378  
Db 400 VFEHMEQCAVKLAKWGVYSAGTVEYLYS-QDRSFYFLELNPRLQVEHPCTEMVADVNL 458  
Qy 379 AAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDDFSSPESFQTKRKPQPOGHVACRIT 438  
Db 459 AAQLQIANGIPLYRIKDIRMMYGVSPWGDSPIDFDSA-----HVPCPRGHVIAARIT 511  
Qy 439 AENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEAR 498  
Db 512 SENPDEGFKPSSGTVOELNFRSNKNVWGYFSVAAAGLHEFADSFQGHCFSGWESREEAI 571  
Qy 499 KQMVISLKELSIRGDFRTTVEYLYKLETDAFESNKITTGWLDGLIQDRLTAERPPADLA 558  
Db 572 SNMVVALKELSIRGDFRTTVEYLYKLETTESFQMNRIIDTGWLDRLIAEKVQAEPRDPTMLG 631  
Qy 559 V 559  
Db 632 V 632

RESULT 8  
I38928  
acetyl-CoA carboxylase (EC 6.4.1.2), hepatic - human  
N;Alternate names: acetyl-Coenzyme A carboxylase  
C;Species: Homo sapiens (man)  
C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: I38928  
R;Abu-Elheiga, L.; Jayakumar, A.; Baldini, A.; Chirala, S.S.; Wakil, S.J.  
Proc. Natl. Acad. Sci. U.S.A. 92, 4011-4015, 1995  
A;Title: Human acetyl-CoA carboxylase: characterization, molecular cloning, and evidence  
A;Reference number: I38928; MUID:95249602; PMID:7732023  
A;Accession: I38928  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2346 <RES>  
A;Cross-references: UNIPROT:Q13085; UNIPARC:UPI0000127C6D; EMBL:U19822; NID:g849082; PID  
A;Experimental source: HepG2 cells  
C;Genetics:  
A;Gene: ACC  
A;Map position: 17q12  
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-  
C;Keywords: biotin binding; ligase; liver  
F;120-620/Domain: biotin carboxylase homology <BCH>  
F;747-819/Domain: lipoyl/biotin-binding homology <LPB>  
F;786/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 61.3%; Score 1781; DB 2; Length 2346;  
Best Local Similarity 63.6%; Pred. No. 5.2e-118;  
Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;  
Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAIVKVEIRSKWAYETFGDERAIEFTVMATPED 81  
Db 103 ASP-AEFVTRFGGNKLVIEKVLINNGIAAIVKCMRSIRRSWSYEMFERNERAIRFVVMVTPED 161  
Qy 82 LKVNADYIRMAQDYVEVPGGSSNNNNYANVDLIVDAERAGVHA VVAGWGHASENPRLPES 141  
Db 162 LKANA EYIKWADHYVPVPGGANNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL 221  
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVQAQHADVPCMPWSGTGKETMMSD---QGFL 198  
Db 222 LL--KNGIAFMGPPNQAMWALGDKIASSIVAQTAGIPTLPWSGSLRVDMQENDFSKRIL 279

Qy 199 TVSDVVYQACIHTAEEGLEKAEGKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258  
Db 280 NVPQELYEGYVKDVGDLQAEEVGYPMIKASEGGGKGIRKVNADDFPNLFRQVQA 339  
Qy 259 EVPGPSVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEAPVTIAPED 318  
Db 340 EVPGPSIFVMRLAKQSRHLEVQILADQYGNNAISLFGDCSVQRRHQKIIIEAPATIATPA 399  
Qy 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378  
Db 400 VFEHMEQCAVKLAKWGVYSAGTVEYLYS-QDGSFYFLELNPRLQVEQPCTEMVADVNL 458  
Qy 379 AAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDDFSSPESFQTKRKPQPOGHVACRIT 438  
Db 459 AAQLQIANGIPLYRIKDIRMMYGVSPWGDSPIDFENSA-----HVPCPRGHVIAARIT 511  
Qy 439 AENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEAR 498  
Db 512 SENPDEGFKPSSGTVOELNFRSNKNVWGYFSVAAAGLHEFAGSFQGHCFSGWENREEAI 571  
Qy 499 KQMVISLKELSIRGDFRTTVEYLYKLETDAFESNKITTGWLDGLIQDRLTAERPPADLA 558  
Db 572 SNMVVALKELSIRGDFRTTVEYLYKLETTESFQMNRIIDTGWLDRLIAEKVRAERPDPTMLG 631  
Qy 559 V 559  
Db 632 V 632

RESULT 9  
A29924  
acetyl-CoA carboxylase (EC 6.4.1.2), hepatic - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A29924; A29337; A27903  
R;Takai, T.; Yokoyama, C.; Wada, K.; Tanabe, T.  
J. Biol. Chem. 263, 2651-2657, 1988  
A;Title: Primary structure of chicken liver acetyl-CoA carboxylase deduced from cDNA s  
A;Reference number: A29924; MUID:88139305; PMID:2893793  
A;Accession: A29924  
A;Molecule type: mRNA  
A;Residues: 1-2324 <TAK1>  
A;Cross-references: UNIPROT:P11029; UNIPARC:UPI0000127CAB; GB:J03541; NID:g211567; PID  
R;Takai, T.; Wada, K.; Tanabe, T.  
FEBS Lett. 212, 98-102, 1987  
A;Title: Primary structure of the biotin-binding site of chicken liver acetyl-CoA carb  
A;Reference number: A91375; MUID:87106011; PMID:2879745  
A;Accession: A29337  
A;Molecule type: mRNA  
A;Residues: 493-820 <TAK2>  
A;Cross-references: UNIPARC:UPI0000171282; GB:X05019; NID:g63021; PIDN:CAA28675.1; PID  
A;Accession: A27903  
A;Molecule type: mRNA  
A;Residues: 493-552,554-783,'RSPS',789-820 <TAK3>  
A;Cross-references: UNIPARC:UPI000017312E  
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti  
C;Keywords: biotin binding; ligase; liver  
F;120-620/Domain: biotin carboxylase homology <BCH>  
F;747-819/Domain: lipoyl/biotin-binding homology <LPB>  
F;786/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 61.2%; Score 1780; DB 1; Length 2324;  
Best Local Similarity 63.4%; Pred. No. 6e-118;  
Matches 343; Conservative 81; Mismatches 103; Indels 14; Gaps 5;  
Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAIVKVEIRSKWAYETFGDERAIEFTVMATPED 81  
Db 103 ASP-AEFVTRFGGNRVIEKVLINNGIAAIVKCMRSIRRSWSYEMFERNERAIRFVVMVTPED 161  
Qy 82 LKVNADYIRMAQDYVEVPGGSSNNNNYANVDLIVDAERAGVHA VVAGWGHASENPRLPES 141  
Db 162 LKANA EYIKWADHYVPVPGGPNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL 221







Db 110 VNGYHSDVVPGRNVAEVEFCKALGGKRPISILVATNGMAAVKFIRSVRTWAYETFGSE 169

QY 69 RAIEFTVMATPEDLKVNADYIRMADQYVEVPGSSNNNNYANVDLIVDVAERAGVH 128

Db 170 KAVKLVMATPEDMRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEMAEVTRVD 229

QY 129 WGHASENPRLPESLAASKHK- IIFIGPPGSAMRSLGDKISSITIVAQAHDVPCMPWSGTGI 187

Db 230 WGHASENPELDAAL---KEKGIIFLGPPADSMIALGDKIGSSLIAQAADVPTLPWSGSHV 286

QY 188 KETMMSDQGLTVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGE 247

Db 287 K--IPPGRLVTPVEEIKKACVYTTTEEAATASCQVVGYPAMIKASWGCGGKGIRKVHND 344

QY 248 EFQQLYNALGVEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKII 307

Db 345 EVRALFKVQGEVPGSPIFIMKVASQSRHLEAQLLCDQYGNVAALHSRDCSVQRRHQKII 404

QY 308 EEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVVWLYSPESGEFAFLELNPRLQVEHP 367

Db 405 EEGPITVAPQETIKKLEQARRLAKSVNYVGAATVEYLYSMDTGEYFLELNPRLQVEHP 464

QY 368 TTEMVSGVNIPAAQLQVAMGIPLYISIRDIRTYLGMDFRG-----NEVI--DFDESSPE 418

Db 465 VTEWIAEVLNPAQVAVGMGIPLWQIPEIRRFYGMHGGGYDSWRKTSVVASPFDFDEAE 524

QY 419 SFKTQRPQPOGHVACRITAENPDGTGFKPGMGALTELNFRSSTWGYFSVGTSGALHE 478

Db 525 SLR-----PKGHCVAVRVTSEDPPDGFKPTSQEIQELSFKSKPNMWSYFSVKSGGIHE 578

QY 479 YADSQFG-----HIFAYGADRSEARKQMVISLKELSIKIRGDFRTTVEYLIKLEL 527

Db 579 FSDSQFGKLNKFGMLGQHVAFGESRSVAIANMVLALKEIQIRGDIRTNVDYITDLLHA 638

QY 528 DAFESNKITTGWLDGLIQDRLTAERPDLAV 559

Db 639 SDYRENKIHTGWLDSRIAMRVRAERPWWYLSV 670

RESULT 14

D86483

protein F5J5.19 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: D86483

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86483

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2257 <STO>

A:Cross-references: UNIPROT:Q9SKV1; UNIPARC:UPI00000A0B33; GB:AE005172; NID:g12039052; P

C:Genetics:

A:Gene: F5J5.19

A:Map position: 1

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

Query Match 54.3%; Score 1579; DB 2; Length 2257;

Best Local Similarity 53.5%; Pred. No. 1.2e-103;

Matches 302; Conservative 96; Mismatches 143; Indels 24; Gaps 5;

QY 4 DHKAVSQFIGGNPLETAPASPVADFIRKQGGHVSITKVLICNNGIAAVKEIRSIRKWAYE 63

Db 8 NHSAV-----GPGINYETVSQVDFCKALRGKRPISILIANNGMAAVKFIRSVRTWAYE 62

QY 64 TFGDERAJEFTVMATPEDLKVNADYIRMADQYVEVPGSSNNNNYANVDLIVDVAERAGVH 123

Db 63 TFGTEKAILLVGMATPEDMRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEMAEVTRVD 122

QY 124 AVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQAHDVPCMPWS 183

Db 123 AVWPGWGHASENPELDAK--GIIFLGPPASSMAALGDKIGSSLIAQAADVPTLPWS 180

QY 184 GTCIKETMMSDQGLTVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKC 243

Db 181 GSHVK--IPPSNLVTPIPEIYRQACVYTTTEEAIASCQVVGYPAMIKASWGCGGKGIRKV 238

QY 244 TNGEEFKQLYNALGVEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRH 303

Db 239 HNDDEVRLFKVQGEVPGSPIFIMKVASQSRHLEVQLLCKHGNVSALHSRDCSVQRRH 298

QY 304 QKIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVVWLYSPESGEFAFLELNPRLQ 363

Db 299 QKIEEGPITVAPPETVKKLEQAARRLAKSVNYVGAATVEYLYSMDTGEYFLELNPRLQ 358

QY 364 VEHTTEMVSGVNIPAAQLQVAMGIPLYISIRDIRTYLGMDFRGN-----EVIDFDF 414

Db 359 VEHPTWEIAEINLPAAQVAVGMGIPLWQIPEIRRFYGHGGGYDSWRKTSVVAFFPDF 418

QY 415 SSPESFKTQRPQGHVACRITAENPDGTGFKPGMGALTELNFRSSTWGYFSVGTSG 474

Db 419 DKAQSIR-----PKGHCVAVRVTSEDPPDGFKPTSQSRVQELSFKSKPNVWAYFSVKSGG 472

QY 475 ALHEYADSQFCHIFAYGADRSEARKQMVISLKELSIKIRGDFRTTVEYLIKLELDAFESNK 534

Db 473 GIHEFSDSQFCHVAFGESRALAIANMVLGLKEIQIRGEIRTNVDYITDLLHASDYRDNK 532

QY 535 ITTGWLDGLIQDRLTAERPDLAV 559

Db 533 IHTGWLDSRIAMRVRAERPWWYLSV 557

RESULT 15

T09538

acetyl-CoA carboxylase (EC 6.4.1.2) - alfalfa

C:Species: Medicago sativa (alfalfa)

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C:Accession: T09538

R:Shorrosh, B.S.; Dixon, R.A.; Ohlrogge, J.B.

Proc. Natl. Acad. Sci. U.S.A. 91, 4323-4327, 1994

A>Title: Molecular cloning, characterization, and elicitation of acetyl-CoA carboxylas

A:Reference number: A58381; MUID:94240129; PMID:7910406

A:Accession: T09538

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-2257 <SHO>

A:Cross-references: UNIPROT:Q40326; UNIPARC:UPI000009D22E; EMBL:L25042; NID:g495724; P

A:Experimental source: substrain sativa, cultivar Apollo; callus

C:Genetics:

A:Gene: ACCase

C:Function:

A:Description: catalyzes ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA

A:Pathway: fatty acid biosynthesis

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti

C:Keywords: ligase

F:41-547/Domain: biotin carboxylase homology <BCH>

F:674-746/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 54.3%; Score 1577.5; DB 2; Length 2257;

Best Local Similarity 54.3%; Pred. No. 1.5e-103;

Matches 298; Conservative 93; Mismatches 139; Indels 19; Gaps 4;

QY 20 APASPVADFIRKQGGHVSITKVLICNNGIAAAKEIRSIRKWAYETFGDERAIEFTVMATP 79

Db 21 ATTEVDEYCNALGGNKPIHISILIANNGMAAVKFIRSVRSWAYETFGTEKAILLVAMATP 80

QY 80 EDLKNADYIRMADQYVEVPGSSNNNNYANVDLIVDVAERAGVHVAWGWHASENPRLP 139







C;Genetics:  
A;Gene: ACCase-B  
A;Introns: 116/3; 185/3; 239/3; 270/3; 302/3; 360/3; 391/3; 454/3; 471/3; 484/3; 526/3; 5/3; 1464/3; 1524/3  
C;Function:  
A;Description: catalyzes ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA  
A;Pathway: fatty acid biosynthesis  
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-  
C;Keywords: ligase  
F;41-547/Domain: biotin carboxylase homology <BCH>  
F;674-746/Domain: lipoyl/biotin-binding homology <LPB>  
  
Query Match 53.5%; Score 1555.5; DB 2; Length 1978;  
Best Local Similarity 53.2%; Pred. No. 4.6e-102;  
Matches 291; Conservative 100; Mismatches 141; Indels 15; Gaps 4;  
  
Qy 20 APASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP 79  
Db 21 AAISEVDDFCNALCGNRPIHSILIANNGMAAVKFIRSVRSWAYETFGSEKAILLVAMATP 80  
  
Qy 80 EDLKVADYIRMAQDYVEVPGGSSNNNNYANVDLIVDAERAGVHVAWAGHASENRLP 139  
Db 81 EDMRINAEHRIADQFAEVPGGTNNNNYANVQLILEMAEITHVDVAVPWGWHASENPELP 140  
  
Qy 140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLT 199  
Db 141 DALKAK--GIVFLGPPAISMALGDKIGSSLIAQAAAEVTLPLWSGSHVK--IPPESSLIT 196  
  
Qy 200 VSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFQKOLYNALGE 259  
Db 197 IPDEIYREACVYTTTEAVASCQVVGYPAMIKASWRGGKGIRKVHNDDEVRLFQKQVGE 256  
  
Qy 260 VPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHOKIIEEAPVTIAPEDA 319  
Db 257 VPGSPFIMKVASQSRHLEVQLLADQYGNVAALHSRDCSIQRRYQKIIEEGPITVAPIET 316  
  
Qy 320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPVTTEMVSGVNIPA 379  
Db 317 VKQLEQAARRLAKSVNYGAAATVEYLFMETGEYFLELNPRLQVEHPVTWIAEINLPA 376  
  
Qy 380 AQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFD-----FSSPESFKTQKQPQGHV 432  
Db 377 AQVAIGMGIPLWQIPEIRRFYGVHEGG-----YDAWRKTSVLATPFDKQAQSTRPKGHC 432  
  
Qy 433 VACRTAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGA 492  
Db 433 VAVRVTSEDDPDGFKPTSGKVQELSPKSNVWAYFSVKSGGHIHFSDSQFGHVFAGE 492  
  
Qy 493 DRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGLIQDRLTAER 552  
Db 493 SRALTIANMVLGLKEIQIRGEIRTNVDYTIDLLNASDYRENKIHTGWLDSRIAMRVRAER 552  
  
Qy 553 PPADLAV 559  
Db 553 PPWYLSV 559

RESULT 20  
T02235  
acetyl-CoA carboxylase (EC 6.4.1.2) - maize  
N;Alternate names: acetyl-coenzyme A carboxylase  
C;Species: Zea mays (maize)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T02235  
R;Eglin, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.  
Plant Physiol. 108, 1299-1300, 1995  
A;Title: A maize acetyl-coenzyme A carboxylase cDNA sequence.  
A;Reference number: Z14632; MUID:95357420; PMID:7630949  
A;Accession: T02235  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2325 <EGL>  
A;Cross-references: UNIPROT:Q41743; UNIPARC:UPI00000A4B72; EMBL:U19183; NID:g1045304; PI

A;Experimental source: strain A188; leaf  
C;Function:  
A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA  
A;Pathway: fatty acid biosynthesis  
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-  
C;Keywords: ligase  
F;134-640/Domain: biotin carboxylase homology <BCH>  
F;767-839/Domain: lipoyl/biotin-binding homology <LPB>  
  
Query Match 53.1%; Score 1543.5; DB 2; Length 2325;  
Best Local Similarity 53.5%; Pred. No. 4.2e-101;  
Matches 294; Conservative 94; Mismatches 141; Indels 21; Gaps 5;  
  
Qy 20 APASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP 79  
Db 114 ASVSKVVEFCAALGGKTPHISILVANNGMAAAKFMRSVRTWANDTFGSEKAIQLIAMATP 173  
  
Qy 80 EDLKVADYIRMAQDYVEVPGGSSNNNNYANVDLIVDAERAGVHVAWAGHASENRLP 139  
Db 174 EDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVGMAQKLGVSVAWPWGWHASENPELP 233  
  
Qy 140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGK---ETMMSDQ 196  
Db 234 DALTA--GIVFLGPPASSMNALGDKVGSALIAQAAGVPTLAWSGSHVEVPLECCLD--- 288  
  
Qy 197 FLTVDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFQKOLYNALV 256  
Db 289 --AIPEEMYRKACVTTTEEAVASCQVVGYPAMIKASWGGGKGIRKVHNDDEVRLFQKV 346  
  
Qy 257 LGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHOKIIEEAPVTIAP 316  
Db 347 QGEVPGSPFIMRLASQSRHLEVQLLADQYGNVAALHSRDCSVQRRHOKIIEEGPVTVP 406  
  
Qy 317 EDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPVTTEMVSGVN 376  
Db 407 RETVKALEQAARRLAKAVGYGAATVEYLYSMETGDYVYFLELNPRLQVEHPVTWIAEIVN 466  
  
Qy 377 IPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFD-----FSSPESFKTQKQPQ 429  
Db 467 LPAAQVAVGMGIPLWQIPEIRRFYGM DYGG-----YDIWRKTAALATPFNFDEVD SQWPK 522  
  
Qy 430 GHVACRTAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFA 489  
Db 523 GCHVAVRITSEDDPDGFKPTSGKVKEISFKSKPNVWAYFSVKSGGHIHFADSQFGHAF 582  
  
Qy 490 YGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGLIQDRLT 549  
Db 583 YGLSRPAAITNMSLALKEIQIRGEIHSNVDYTVDLLNASDFRENKIHTGWLDTRIAMRVQ 642  
  
Qy 550 AERPPADLAV 559  
Db 643 AERPPWYISV 652

RESULT 21  
A48757  
acetyl-CoA carboxylase (EC 6.4.1.2) - Cyclotella cryptica  
C;Species: Cyclotella cryptica  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A48757  
R;Roessler, P.G.; Ohlrogge, J.B.  
J. Biol. Chem. 268, 19254-19259, 1993  
A;Title: Cloning and characterization of the gene that encodes acetyl-coenzyme A carbo-  
A;Reference number: A48757; MUID:93374903; PMID:8103514  
A;Accession: A48757  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-2089 <ROE>  
A;Cross-references: UNIPROT:Q39478; UNIPARC:UPI00000A5A26; GB:L20784; NID:g1065903; PI  
A;Note: authors translated the codon GGC for residue 1834 as Ala  
C;Genetics:  
A;Introns: 25/1; 729/1  
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-



QY 82 LKVNADYIRMADQYVEVPVGGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141  
Db 74 MRSASHYLKLADETVMAPAGSNKFNCDVIRLAVEAQVDAVYVWGHASENPCLRR 133  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSITIVAHADVPCMPWSGTGK-ETMMSDQGLTV 200  
Db 134 L--ELNNIIFIGPSEKSIASGDKIVSTIIAIGMPTVTWTGSGVKVEECVDFEY--- 188  
QY 201 SDDVYQQACIHTAEGLKAEK--IGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258  
Db 189 -HELRSKATIRNVKEGLEAIEKYGIGVPMIKASEGGGKGIRKCTNGEEFKQLFKEVEL 247  
QY 259 EVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEEAPVTIAPED 318  
Db 248 EFPNSPIFLMKMCDGARHVEIQILGDKHGVIALSSRDCTIQRRCQKVEIEEAPASIVPGE 307  
QY 319 ARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378  
Db 308 VMQMKKDALAFANFVGYYSAGTVLELLFIPTNEYFFLELNPRLQVEHPCTESICDVNP 367  
QY 379 AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFESSPESFQTKRQPQ--HVVACR 436  
Db 368 ALQYQIAMGRKLDIPCIKFREREATGN-----AGGVHCHMAAR 406  
QY 437 ITAENPDTGFXPGMGALTELNFRSSSTWGYFSVGTSGALHEYADSQFGHIPAYGADRSE 496  
Db 407 VTCEDPNDRLEPSTGTVRSCLKFNSTSKAWAYFSLSDGSTVHEFADSQIGHVFARGDRNE 466  
QY 497 ARKQMVISLKELSIKIRGDFRTTVEYLKLETDAPESNKITTGWLDGLIQDR 547  
Db 467 AIANLKHGLQNLKIDATFTPTQSDYLIDLLSLEKFKSNQYDTQWLDKRIASK 517  
RESULT 24  
T07938  
probable acetyl-CoA carboxylase (EC 6.4.1.2), chloroplast - rape (fragment)  
C;Species: Brassica napus (rape)  
C;Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
C;Accession: T07938  
R;Schulte, W.  
submitted to the EMBL Data Library, December 1996  
A;Reference number: Z16232  
A;Accession: T07938  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-371 <SCH>  
A;Cross-references: UNIPROT:O04850; UNIPARC:UPI000009F1F2; EMBL:Y10302; PIDN:CAA71347.1  
A;Experimental source: cv. Akela  
C;Genetics:  
A;Genome: nuclear  
A;Introns: 100/1; 213/3; 282/3; 336/3; 367/3  
C;Function:  
A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA  
A;Pathway: fatty acid biosynthesis  
A;Note: probably chloroplast isoform  
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-  
C;Keywords: chloroplast; ligase  
Query Match 26.5%; Score 769; DB 2; Length 371;  
Best Local Similarity 51.9%; Pred. No. 3.9e-47;  
Matches 138; Conservative 57; Mismatches 67; Indels 4; Gaps 2;  
QY 12 IGGNPLETAPASPVADFIRKQGHSHVITKVLICNNNGIAAVKEIRSIRKWAYETFGDERAI 71  
Db 110 INGNDSAVRVSQVDEFCCKAHGKRPISILVATNGMAAVKLIRSVRAWSYQTFGSEKSI 169  
QY 72 EFTVMATPEDLKNADYIRMADQYVEVPVGGSSNNNNYANVDLIVDAERAGVHAVWAGWGH 131  
Db 170 SLVAMATPEDMRINAEHRIADQFMQVPGGTNNNNYANVHLIVEMAQATGVDVWPVGWGH 229  
QY 132 ASENRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAHADVPCMPWSGTGKETM 191  
Db 230 ASENPELPDALKAK--GVIFLGPTAASMLALGDKIGSSLLIAQAADVPTLPWSGSHVK--I 285

QY 192 MSDQGLTVSDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQ 251  
Db 286 PPGSSMVTIPEEMYRQACVYTTTEAVASCQVVGYPAMIKASWGSGKGIREVHDDDEVRT 345  
QY 252 LYNNAVLEVPVGPSPVFMKLAGQARHL 277  
Db 346 LFKVQGEVPVGPSPIFIMKVASQSRHL 371  
RESULT 25  
A69123  
biotin carboxylase - Methanobacterium thermoautotrophicum (strain Delta H)  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: A69123  
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.  
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني,  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fun  
A;Reference number: A69000; MUID:98037514; PMID:9371463  
A;Accession: A69123  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-491 <MTH>  
A;Cross-references: UNIPROT:O27939; UNIPARC:UPI0000132BC1; GB:AE000942; GB:AE000666; N  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH1917  
C;Superfamily: biotin carboxylase; biotin carboxylase homology  
F;4-450/Domain: biotin carboxylase homology <BCH>

Query Match 24.9%; Score 724; DB 2; Length 491;  
Best Local Similarity 34.4%; Pred. No. 9.5e-44;  
Matches 179; Conservative 89; Mismatches 158; Indels 94; Gaps 14;  
QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYV 96  
Db 1 MFSKILVANRGEIAIRVMRACRELGIKS-----VAVYSEADKNALFTRYADEAY 49  
QY 97 EVPGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG 156  
Db 50 EIGKPAPSQSYLRIDRILEVAEKAGAEIHPGYFLAENPRLEE--CEKQIGKILIGPKG 107  
QY 157 SAMRSLGDKISSITIVAHADVPCMPWSGTGKETMMSDQGLTVSDDVYQQACIHTAEEG 216  
Db 108 SVIEAMGDKITSKLKKKAGVPVIP--GT-----DQG---VSD-----PDEA 144  
QY 217 LEKAEKIGYPVMIKASEGGGKGIRKCTNGEEF---KQLYNNAVLEVPVGPSP-VFVMKLAG 272  
Db 145 ARIADSIGYPVVIKASAGGGGIGMRAVYEEDELIRAMESTQSVAAAFGDPFTVYIEKYLE 204  
QY 273 QARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAK 332  
Db 205 RPRHIEFQVMADESGNVHLADRECSIQRRHQKLEIEAPSPIMTPELRERMGSAAVKAEE 264  
QY 333 LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYS 392  
Db 265 YIGYENAGTVEFLYS--NGDFYFLEMNTRIQVEHPITEVITGVDLVKEQIRVASG----- 317  
QY 393 IRDITLYGMDPRGNEVIDDFESSPESFQTKRQPQPOGHVVACRITAENPDTGFKPGMGA 452  
Db 318 -----EELRF-----TKDINIRGHAIECRINAENPLADFAPNPGK 353  
QY 453 LTELNFRSSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKOM 501  
Db 354 IT-----GYRSPGGIGVRVDSGVYVMYIEPPFYDSMISKLIWGMDRQEAENRM 402  
QY 502 VISLKELSIKIRGDFRTTVEYLKLETDAPESNKITTGWLD 541  
Db 403 KRALSEYIILG-VKTTIPFHKAIRNEAFRRRGELHPTHFVD 441



RESULT 26  
AH1923  
biotin carboxylase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AH1923  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AH1923  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-447 <KUR>  
A;Cross-references: UNIPROT:Q06862; UNIPARC:UPI00001251AA; GB:BA000019; PIDN:BAB72896.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: accC  
C;Superfamily: biotin carboxylase; biotin carboxylase homology

Query Match 24.4%; Score 709.5; DB 2; Length 447;  
Best Local Similarity 32.9%; Pred. No. 9e-43;  
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;  
  
QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVP 99  
Db 5 KILIANRGEIALRILRACEEMGIATI----AVHSTV-----DRNALHVQLADEAVCIG 53  
  
QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159  
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGTPTPEAI 111  
  
QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLK 219  
Db 112 RLMGDKSTAKETMQAGVPTVPGS-----EGLVETEQEGLEL 148  
  
QY 220 AEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVGLGEV----PGSPVFMVKLAGQAR 275  
Db 149 AKDIGYPVMIKATAGGGGRMRLVRSDFVKFLFLAAQGEAGAAFGNAGVYIEKFIERPR 208  
  
QY 276 HLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335  
Db 209 HIEFQILADNYGNVHILGERDCSIQRRNQKLEEPSALDSDLREKMGQAAVKAQFIN 268  
  
QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395  
Db 269 YTGAGTIEFLLD-RSGQFYFMEMNTRIQVEHPVTEMVTGVDLLVEQIRIAQGERLRLTQD 327  
  
QY 396 IRTLYGMDPRGNEVIDFDESSPESFKTQKPPQGHVVACRITAENPDFTGFKPGMGALTE 455  
Db 328 QVVL-----RGHAIECRINAEDPDHDFRPAPGRIS- 357  
  
QY 456 LNFRSSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGVGRIDSHVYTDYQIPPPYDSLIGKLIWGPDRATAINRMKRA 407  
  
QY 505 LKELSIRGDFRTTVEYLKLETDAPESNKITTTGWL 540  
Db 408 LRECAITG-LPTTIGFHORIMENPQFLQGNVSTSFV 442

RESULT 27  
A53311  
biotin carboxylase (EC 6.3.4.14) - Anabaena sp. (strain PCC 7120)  
N;Alternate names: acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase chain  
C;Species: Anabaena sp.  
C;Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: A53311  
R;Gornicki, P.; Scappino, L.A.; Haselkorn, R.  
J. Bacteriol. 175, 5268-5272, 1993

A;Title: Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena sp. strain  
A;Reference number: A53311; MUID:93352435; PMID:8102363  
A;Accession: A53311  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-447 <GOR>  
A;Cross-references: UNIPROT:Q06862; UNIPARC:UPI00001251AA; GB:114862; NID:g289132; PID:  
C;Superfamily: biotin carboxylase; biotin carboxylase homology  
C;Keywofds: ATP; ligase  
F;5-447/Domain: biotin carboxylase homology <BCH>

Query Match 24.4%; Score 709.5; DB 2; Length 447;  
Best Local Similarity 32.9%; Pred. No. 9e-43;  
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;  
  
QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVP 99  
Db 5 KILIANRGEIALRILRACEEMGIATI----AVHSTV-----DRNALHVQLADEAVCIG 53  
  
QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159  
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGTPTPEAI 111  
  
QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLK 219  
Db 112 RLMGDKSTAKETMQAGVPTVPGS-----EGLVETEQEGLEL 148  
  
QY 220 AEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVGLGEV----PGSPVFMVKLAGQAR 275  
Db 149 AKDIGYPVMIKATAGGGGRMRLVRSDFVKFLFLAAQGEAGAAFGNAGVYIEKFIERPR 208  
  
QY 276 HLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335  
Db 209 HIEFQILADNYGNVHILGERDCSIQRRNQKLEEPSALDSDLREKMGQAAVKAQFIN 268  
  
QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395  
Db 269 YTGAGTIEFLLD-RSGQFYFMEMNTRIQVEHPVTEMVTGVDLLVEQIRIAQGERLRLTQD 327  
  
QY 396 IRTLYGMDPRGNEVIDFDESSPESFKTQKPPQGHVVACRITAENPDFTGFKPGMGALTE 455  
Db 328 QVVL-----RGHAIECRINAEDPDHDFRPAPGRIS- 357  
  
QY 456 LNFRSSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGVGRIDSHVYTDYQIPPPYDSLIGKLIWGPDRATAINRMKRA 407  
  
QY 505 LKELSIRGDFRTTVEYLKLETDAPESNKITTTGWL 540  
Db 408 LRECAITG-LPTTIGFHORIMENPQFLQGNVSTSFV 442

RESULT 28  
H81978  
probable acetyl-CoA carboxylase (EC 6.4.1.2) biotin carboxylase chain NMA0596 [similar:  
N;Contains: biotin carboxylase (EC 6.3.4.14)  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: H81978  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mori  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A;Reference number: A81775; MUID:20222556; PMID:10761919  
A;Accession: H81978  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-453 <PAR>  
A;Cross-references: UNIPROT:Q9JW07; UNIPARC:UPI00000C49E5; GB:AL162753; GB:AL157959; N:  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: accC; NMA0596  
C;Superfamily: biotin carboxylase; biotin carboxylase homology

C;Keywords: ligase

Query Match 23.4%; Score 679; DB 2; Length 453;  
Best Local Similarity 32.6%; Pred. No. 1.4e-40;  
Matches 170; Conservative 90; Mismatches 176; Indels 86; Gaps 13;

QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYV 96  
Db 1 MLKKVLIANRGEIALRVLRACREMGIAI-----VAVHSEADKDSLHVKLADESV 49  
QY 97 EVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHIIIFIGPPG 156  
Db 50 CIGPAASAQSYLVNPAIAAAEVSCADAVHPGYGFLAENADFAEQVEQS--GFTFIGPKP 107  
QY 157 SAMRSLGDKISSITIVAQHADVPCMPWPGTGKIKETMMSDQGFLLTVSDVYQQACIHTAEEG 216  
Db 108 DTIRLMGDKVSAKHAMIAAGVPCVPGS-----DGALPDDG-----EEI 145  
QY 217 LEKAEKIGYPMIKASEGGGKGIRKCTNGEEFKQ---LYNAVLEVPVGPSP-VFVMKLAG 272  
Db 146 LKIADKIGYPMIKASEGGGKGIRKCTNGEEFKQ---LYNAVLEVPVGPSP-VFVMKLAG 272  
QY 273 QARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIEEAPVTIAPEDARESMEKAAVRLAK 332  
Db 206 RPRHVEIQVIADEHGNVAVYLAERDCSLQRRHQKIEEAPVTIAPEDARESMEKAAVRLAK 332  
QY 333 LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTMMVSGVNIIPAAQLQVAMGIPL-Y 391  
Db 266 RIGYRGAGTFFELY--EDGEFFFIEMNTRVQVEHPVTELITGVDIVQEQLRIAGLPLQY 323  
QY 392 SIRDIRTLYGMDPRGNEVIDDFSSPESFQTKRQKPOQGHVACRITAENPDGTGFKPGMG 451  
Db 324 KQKDI-----QVEGHAFECRINAEDP--YNFIPSPG 352  
QY 452 ALTELNFRSSTSTWGYFSVGTSGALHE-----YADSQFGHIFAYGADRSEARKQMVISL 505  
Db 353 PIESCHLPSG-----FGIRVDSHIYQYRIPPYDLSLIGKVCVVGKDRDQAMAKMRVAL 406  
QY 506 KELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGLQDR 547  
Db 407 AELAITG-IKNTPLHRDLFNDPGFKQGGVSIHYLEHWLEDR 447

RESULT 29

A69581  
acetyl-CoA carboxylase (biotin carboxylase subunit) accC - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: A69581  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillette, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, K.; Yata, K.; Yoshida, K.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: A69581  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-450 <KUN>  
A;Cross-references: UNIPROT:P49787; UNIPARC:UPI00000606EA; GB:Z99116; GB:AL009126; NID:9  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: accC

C;Superfamily: biotin carboxylase; biotin carboxylase homology  
F;4-450/Domain: biotin carboxylase homology <BCH>

Query Match 23.3%; Score 676; DB 2; Length 450;  
Best Local Similarity 33.2%; Pred. No. 2.2e-40;  
Matches 172; Conservative 81; Mismatches 177; Indels 88; Gaps 12;

QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYV 96  
Db 1 MIKKLLIANRGEIAVRIIRACRELGIET-----VAVYSEADKDALHVQMADEAF 49  
QY 97 EVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHIIIFIGPPG 156  
Db 50 CIGPKASKDSYLVNVTNIVSVAKLTGTDAIHPGYGFLAENADFAE--LCEEVNVTVFGPSP 107  
QY 157 SAMRSLGDKISSITIVAQHADVPCMPWPGTGKIKETMMSDQGFLLTVSDVYQQACIHTAEEG 216  
Db 108 DAISKMGTKDVARETMKQAGVPIVPGS-----QGIENVEEA 144  
QY 217 LEKAEKIGYPMIKASEGGGKGIR-----KCTNGEEFKQLYNAVLEVPVGPSPVFVMKL 270  
Db 145 VSLANEIGYPMIKASEGGGKGIRVARTEEELINGIKITQOEATAFRNPG--VYIEKY 202  
QY 271 AGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIEEAPVTIAPEDARESMEKAAVRL 330  
Db 203 IEDFRHVEIQVLAADNYGNTIHLGERDCSIQRRQLKEESPSPALDSEIREQMGDAAVKA 262  
QY 331 AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTMMVSGVNIIPAAQLQVAMGIPL 390  
Db 263 AKAVGYTGAGTVEFIYDNEQRYFYMENMTRIQVEHPVTMTGTDLIKEIKVAGSMEL 322  
QY 391 YSIRDIRTLYGMDPRGNEVIDDFSSPESFQTKRQKPOQGHVACRITAENPDGTGFKPGM 450  
Db 323 -SLK-----QEDVEF-----EGWAEICRINAENPSKNFMPSP 353  
QY 451 GALT-----ELNFRSSTSTW-GYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVI 503  
Db 354 GEIKMYLPPGGGLGVVDSAAVPGY-----SIPYYDSMIKAVITYGKTRDEAIARMKR 406  
QY 504 SLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 541  
Db 407 ALSEFVIEG-IETTIPFHLKLEHETFVSGEFNTKFLE 443

RESULT 30

D69277  
biotin carboxylase (acc) homolog - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: D69277  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: D69277  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-506 <KLE>  
A;Cross-references: UNIPROT:O30019; UNIPARC:UPI00000571AD; GB:AE001090; GB:AE000782; N  
C;Superfamily: biotin carboxylase; biotin carboxylase homology  
F;4-450/Domain: biotin carboxylase homology <BCH>

Query Match 23.2%; Score 675; DB 2; Length 506;  
Best Local Similarity 33.7%; Pred. No. 3.1e-40;  
Matches 180; Conservative 83; Mismatches 165; Indels 106; Gaps 18;

QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFG-----DERAIEFTVMATPEDLKNAD---Y 88  
Db 1 MESKILVANRGEIAVRVRACRELGIKTVGVYSSADKRAFH-----RVYADECY 50







Db 356 ATGRLTELSFPEGTSRVD-SGVRQGDITPPYDPLIAKLIVHGQNRSAALGRQLQDALKEC 414

QY 509 SIRGDFRTTVEYLKLETDAPESNKKITTWGLDGLIQDRLTAERPPLAV 559

Db 415 RIGGTV-TNRDFLIRLTHEHDFRSCHPDGTGLIDREI-ERLTAPVAPGDEAL 463

RESULT 35

B64566

biotin carboxylase - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004

C;Accession: B64566

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: B64566

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-458 <TOM>

A;Cross-references: UNIPROT:O25134; UNIPARC:UPI00000D3173; GB:AE000553; GB:AE000511; NID

C;Superfamily: biotin carboxylase; biotin carboxylase homology

F;18-458/Domain: biotin carboxylase homology <BCH>

Query Match 22.8%; Score 662; DB 2; Length 458;

Best Local Similarity 32.1%; Pred. No. 2.2e-39;

Matches 165; Conservative 86; Mismatches 179; Indels 84; Gaps 11;

QY 38 ITKVLICNNGIAA VKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYVE 97

Db 16 LSRILIANRGEIALRAIQTIQEMGKES-----IAIYSIADKDAHYLNTASAKVC 64

QY 98 VPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLPESLAASKHKIIFIGPPGS 157

Db 65 IGGAKSSESYLNPAIISAELFEADAIFPGYGLSENQNFVE--ICSHSLEFIGPSAK 122

QY 158 AMRSLGDKISSTIVAQHADVPCMPWSGTGKETMMSDQGFLTVDVDDVYQACIHTAEGL 217

Db 123 VMALMSDKSKAKSVMEAGMPVIEGSDGLKS-----YGEA-----E 159

QY 218 EKAEGIGYPVMIKASEGGGGKIRKCTNGEEFKQLYNA---VLGEVPGSPVFMKLAGQ 273

Db 160 EIADKIGYPVIAKAAAGGGGRMRVVGDKSLKNLYLAAETEALSAFGSGSVYLEKFINK 219

QY 274 ARHLEVQLLADQYGNASIFGRDCSVQRRHOKIIEEAPVTIAPEDARESMEKAAVRLAKL 333

Db 220 PKHIEVQILADKHGVIHVGERDCSVQRRQQLIIEETPAVLEEGRERLLETAIAKAAKY 279

QY 334 VGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSI 393

Db 280 IGYVGAGTFEFLDSNMKDFYFMEMNTRLQVEHTISEMVSGNLNIEWMIKIAQGEKL--- 336

QY 394 RDIRTLYGMDPRGNEVIDFDFSSPESFKTQRPQGHVVACRITAENPDGTGFKPGMGAL 453

Db 337 -----PKQESFSL-----KGHAIECRITAEDPKK-FYPSPGKI 368

QY 454 TE-----LNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKE 507

Db 369 TEWIAPGGVNVRDLSHAHANYVPT-----HYDSMIGKLIWGENRERARAIAKMKRALKE 422

QY 508 LSIRGDFRTTVEYLKLETDAPESNKKITTWGLD 541

Db 423 FKVEG-IKTTIPFHEMLENADFRQAKIHTKYLE 455

RESULT 36

ABJ352

propionyl-CoA carboxylase (EC 6.4.1.3) [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 31-Dec-2004

C;Accession: AB3352

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite;

A;Reference number: AD3252; PMID:11756688

A;Accession: AB3352

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-667 <KUR>

A;Cross-references: UNIPROT:Q8YHJ8; UNIPARC:UPI0000057E0A; GB:AE008917; PIDN:AAL51981.

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI0800

A;Map position: 1

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti;

C;Keywords: ligase

Query Match 22.7%; Score 660.5; DB 2; Length 667;

Best Local Similarity 32.2%; Pred. No. 5e-39;

Matches 168; Conservative 85; Mismatches 177; Indels 91; Gaps 12;

QY 37 VITKVLICNNGIAA VKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYV 96

Db 1 MIKKILLIANRGEIACRVIKSAKKKIAT-----VAVYSDADRNLHVKMADEAV 49

QY 97 EVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLPESLAASKHKIIFIGPPG 156

Db 50 HIGPAPSNQSYIVIDKILAAIKEIGADAVHPGYGLSENPRFAEALKAA--NVTFIGPPV 107

QY 157 SAMRSLGDKISSTIVAQHADVPCMPWSGTGKETMMSDQGFLTVDVDDVYQACIHTAEEG 216

Db 108 NAIDAMGDKITSKKLAAEAGSVTP-----GHMGLIED-----ADEA 144

QY 217 LEKAEKIGYPVMIKASEGGGGKIRKCTNGEEFKQLYNAVLEVPGS----PVFVMKLAG 272

Db 145 VRIAGSIGYPVMIKASAGGGGKMRIAWDEEAREGFQLSRNEAKSSFQDDRIEFIEKFVT 204

QY 273 QARHLEVQLLADQYGNASIFGRDCSVQRRHOKIIEEAPVTIAPEDARESMEKAAVRLAK 332

Db 205 QPRHIEIQVLGDQHGNNVYLGRECSIQRRNQKIVIEEAPSPFLDEATRKAMGEQAVALAK 264

QY 333 LVGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPL-Y 391

Db 265 AVGYVSAGTVEFIVD-GNRNFYFLEMNTRLQVEHPVTELITGIDLVEEMIRVASGEKLR 323

QY 392 SIRDITLYGMDPRGNEVIDFDFSSPESFKTQRPQGHVVACRITAENPDGTGFKPGMG 451

Db 324 AQADVKL-----NGWAIESRLYAEADPYRNFPLPSIG 353

QY 452 ALTELN-----FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARK 499

Db 354 RLTRYRPPVEGRNPDGTVIRNDT---GVFE---GGEISMYYPDPMIAKLCTWGPDRISAID 407

QY 500 QMVISLKELSIRGDFRTTVEYLKLETDAPESNKKITTWGL 540

Db 408 AMGHALDAFEVEG-IGHNLPFLSAVMDHPRFREGALTTFATFI 447

RESULT 37

C83998

acetyl-CoA carboxylase biotin carboxylase subunit accC [imported] - Bacillus haloduran;

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C;Accession: C83998

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hi; Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: C83998

A;Status: preliminary





Qy	157	SAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLTVSDDVYQQACIHTAEEG	216
Db	108	GAIEAMGDKITSKLAAGVSTVP-----GHMGLIED-----ADEA	144
Qy	217	LEKAEKIGYPMIKASAGGGGKIRKCTNGEEFKOLYNVLGEVPGS----PVFVMKLAG	272
Db	145	VKIASQIGYPMIKASAGGGGKMRIFAEAEAREGFQSSKNEAKSFGDDRIEFKFTV	204
Qy	273	QARHLEVQLLADQYGNASISIFGRDCSVORRHQKIIIEEAPVTIAPEDARESMKAAVRLAK	332
Db	205	QPRHIEIQVLGDKHGTILYLGERECISQRRNQKVEEAPSPFLDEATRHAMGEQAVALAR	264
Qy	333	LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYS	392
Db	265	AVGYHSAGTVEFIVDGER-NFYFLEMTNRLQVEHPVTELVTGIDLVEQMIRVASGEKL--	321
Qy	393	IRDIRTLYGMDPRGNEVIDDFESSPESFKTQPKPOQGHVVACRITAENPDTGFKPGMGA	452
Db	322	-----SLAQGDVVKLN-----GWAIESRLYAEDPYRNFPLPSIGR	354
Qy	453	LTELN-----FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQ	500
Db	355	LTRYRPPGEGAQDSGTVIRNDT---GVFE---GGEISMYYPDPMIAKLCSWGKDRETAIDA	408
Qy	501	MVISLKELSIKRGDRTTVEYLIKLLETDAFESNKITTTGWL-----DGLIQDRLTAER	552
Db	409	MGEALDRFEVEG-IGHNLPFLSAVMQHERFRSRLTTGTGFIAEFPEGFSGIEPDETAARK	467
Qy	553	PPADLAV 559	
Db	468	LSAIAAI 474	

RESULT 40  
AC2997  
hypothetical protein pccA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 31-Dec-2004  
C:Accession: AC2997  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AC2997  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-677 <KUR>  
A:Cross-references: UNIPROT:Q8U924; UNIPARC:UPI00000D2267; GB:AE008689; PIDN:AAL44393.1;  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: pccA  
A:Map position: linear chromosome  
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

Query Match 22.6%; Score 656.5; DB 2; Length 677;  
Best Local Similarity 31.1%; Pred. No. 9.8e-39;  
Matches 170; Conservative 95; Mismatches 185; Indels 97; Gaps 13;

Qy	37	VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPELKNADYIRMADQYV	96
Db	11	MIKKILIANRGEIACRVIKTAKMGIAT-----VAVYSDADANALHVXMADEAV	59
Qy	97	EVPGGSNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG	156
Db	60	HIGPAPSSQSIVIDKILEAIQKTGADAVHPGYGFLSENAFAQAL--EKAGVVFIGPPV	117
Qy	157	SAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLTVSDDVYQQACIHTAEEG	216
Db	118	GAIEAMGDKITSKLAAGVSTVP-----GHMGLIED-----ADEA	154

Qy	217	LEKAEKIGYPMIKASAGGGGKIRKCTNGEEFKOLYNVLGEVPGS----PVFVMKLAG	272
Db	155	VKIASQIGYPMIKASAGGGGKMRIFAEAEAREGFQSSKNEAKSFGDDRIEFKFTV	214
Qy	273	QARHLEVQLLADQYGNASISIFGRDCSVORRHQKIIIEEAPVTIAPEDARESMKAAVRLAK	332
Db	215	QPRHIEIQVLGDKHGTILYLGERECISQRRNQKVEEAPSPFLDEATRHAMGEQAVALAR	274
Qy	333	LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYS	392
Db	275	AVGYHSAGTVEFIVDGER-NFYFLEMTNRLQVEHPVTELVTGIDLVEQMIRVASGEKL--	331
Qy	393	IRDIRTLYGMDPRGNEVIDDFESSPESFKTQPKPOQGHVVACRITAENPDTGFKPGMGA	452
Db	332	-----SLAQGDVVKLN-----GWAIESRLYAEDPYRNFPLPSIGR	364
Qy	453	LTELN-----FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQ	500
Db	365	LTRYRPPGEGAQDSGTVIRNDT---GVFE---GGEISMYYPDPMIAKLCSWGKDRETAIDA	418
Qy	501	MVISLKELSIKRGDRTTVEYLIKLLETDAFESNKITTTGWL-----DGLIQDRLTAER	552
Db	419	MGEALDRFEVEG-IGHNLPFLSAVMQHERFRSRLTTGTGFIAEFPEGFSGIEPDETAARK	477
Qy	553	PPADLAV 559	
Db	478	LSAIAAI 484	

Search completed: February 4, 2006, 18:13:41  
Job time : 50 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 4, 2006, 18:13:07 ; Search time 50 Seconds  
(without alignments)  
924.314 Million cell updates/sec  
Title: US-10-633-835-2  
Perfect score: 2907  
Sequence: 1 PPPDHKAVSQFIGNPLETA.....LDGLIQRLTAERPPADLAV 559  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061.5	70.9	2270	2	US-09-581-909-3
2	2060	70.9	802	2	US-09-433-043B-120
3	2060	70.9	2237	1	US-08-354-973-1
4	1780	61.2	853	2	US-09-433-043B-119
5	1765.5	60.7	852	2	US-09-433-043B-118
6	1578	54.3	2254	1	US-08-677-010-3
7	1578	54.3	2254	1	US-08-790-519-3
8	1577.5	54.3	2257	2	US-09-839-477-8
9	1569.5	54.0	442	2	US-09-248-796A-17027
10	1565	53.8	2257	1	US-08-611-107-10
11	1565	53.8	2257	1	US-08-422-560A-10
12	1565	53.8	2257	2	US-08-468-793-10
13	1547.5	53.2	2311	2	US-08-934-386-9
14	1543.5	53.1	2325	2	US-08-417-089-6
15	1543.5	53.1	2325	2	US-08-695-651-6
16	1543.5	53.1	2325	2	US-08-930-285-6
17	1543.5	53.1	2325	2	US-08-695-421-6
18	1543.5	53.1	2325	2	US-08-697-826A-10
19	1502.5	51.7	2089	1	US-08-418-893D-23
20	1502.5	51.7	2089	1	US-08-418-893D-24
21	1495	51.4	2172	1	US-08-611-107-31
22	1417	48.7	489	2	US-09-631-594-74
23	1265.5	43.5	506	2	US-09-631-594-76
24	1152	39.6	2016	2	US-09-475-252-2
25	963.5	33.1	491	1	US-07-956-700B-109
26	963.5	33.1	491	1	US-08-476-537-109
27	963.5	33.1	491	1	US-08-485-607-109

28	963.5	33.1	491	1	US-08-475-879-109	Sequence 109, App
29	963.5	33.1	491	2	US-09-433-043B-109	Sequence 109, App
30	961.5	33.1	491	2	US-09-433-043B-117	Sequence 117, App
31	709.5	24.4	447	1	US-08-611-107-6	Sequence 6, Appli
32	709.5	24.4	447	1	US-08-422-560A-6	Sequence 6, Appli
33	709.5	24.4	447	2	US-08-468-793-6	Sequence 6, Appli
34	709.5	24.4	593	2	US-09-433-043B-122	Sequence 122, App
35	681.5	23.4	453	1	US-08-611-107-8	Sequence 8, Appli
36	681.5	23.4	453	1	US-08-422-560A-8	Sequence 8, Appli
37	681.5	23.4	453	2	US-08-468-793-8	Sequence 8, Appli
38	679.5	23.4	453	1	US-07-956-700B-6	Sequence 6, Appli
39	679.5	23.4	453	1	US-08-485-607-6	Sequence 6, Appli
40	679.5	23.4	453	1	US-08-475-879-6	Sequence 6, Appli
41	679.5	23.4	453	1	US-08-475-879-6	Sequence 6, Appli
42	679.5	23.4	453	2	US-09-433-043B-6	Sequence 6, Appli
43	679.5	23.4	453	2	US-09-433-043B-121	Sequence 121, App
44	667	22.9	670	2	US-09-328-352-6725	Sequence 6725, Ap
45	663	22.8	1085	2	US-09-248-796A-17494	Sequence 17494, A

ALIGNMENTS

RESULT 1  
US-09-581-909-3  
; Sequence 3, Application US/09581909  
; Patent No. 6566048  
; GENERAL INFORMATION:  
; APPLICANT: Graham Keith DIXON  
; APPLICANT: John Leslie THAIN  
; APPLICANT: John Philip VINCENT  
; APPLICANT: No. 6566048bert Friedemann SCHNELL  
; APPLICANT: Suberna Jini CHAVDA  
; TITLE OF INVENTION: Acetyl-CoA-Carboxylase from Candida Albicans  
; FILE REFERENCE: 009901/0270671 - PJF/PHM70303/UST  
; CURRENT APPLICATION NUMBER: US/09/581,909  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: PCT/GB98/03857  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: GB 9726897.3  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ ID NOS: 3  
; SEQ ID NO 3  
; LENGTH: 2270  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-581-909-3

Query Match	70.9%	Score	2061.5;	DB 2;	Length	2270;
Best Local Similarity	70.7%	Pred. No.	2e-179;			
Matches	390;	Conservative	63;	Mismatches	98;	Indels 1; Gaps 1;
Qy	9	SFIGGNPLETAPASPVADPIRKGHSHVITKVLICNNNGIAAVKEIRSIRKWAYETFGDE	68			
Db	70	SHFLGNSVLNAEPSKVRDFVRAHQGHTVISKILIANNGIAAVKEIRSIRKWAYETFGDE	129			
Qy	69	RAIEFTVMATPEDLVKNADYIRMADQYVEVPGSSNNNNYANVDLIVDAERAGVHAVWAG	128			
Db	130	KAIQFTVMATPEDLEANAIEYRMADQFIEVPGGTNNNNYANVDLIVEIAESTNAHAVWAG	189			
Qy	129	WGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGK	188			
Db	190	WGHASENPLLPKLAASPKIIFIGPPGSAMRSLGDKISSTIVAQHAQVPCIPWSGTGVD	249			
Qy	189	ETWMSDQ-GFLTVDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGE	247			
Db	250	EVKIDPQTNLVSADDIYAKGCTSPEDGLEKAKKIGFPVMIKASEGGGKGIRKVDDEK	309			
Qy	248	EFKQLYNAVLEVPVGFVFMKLAGQARHLEVQLLADQYCNALISIFGRDCSVQRRHQKII	307			
Db	310	NFITLYNQAANEIPGSPIFIMKLAGDARHLEVQLLADQYCNALISIFGRDCSVQRRHQKII	369			
Qy	308	EEAPVTIAPEDARESMEKAARLAKLVGVVSAGTVENWLYSPESGEFAFLELNPRLQVEHP	367			

[illegible]

```

RESULT 2
US-09-433-043B-120
; Sequence 120, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-120

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Query Match	70.9%;	Score 2060;	DB 2;	Length 802;
Best Local Similarity	69.1%;	Pred. No. 5.4e-180;		
Matches 386;	Conservative 76;	Mismatches 89;	Indels 8;	Gaps 3;

  

QY	3	PDHKAVSQFIGGNPLETAPASPVADFI	RKQGGHVSVITKVLICNNGIAA	AAVKEIRSIRKWAY	62	
DB	29	PGH-----FIGLNTVDKLEESPLR	DFVKS	HGGHTVISKILLANNGIAA	AAVKEIRSVRKWAY 83	
QY	63	ETFGDERAIEFTVMATPEDLKNADYI	RMADQYVEVPGGSNNNNYANVD	LI	VDVAERAGV 122	
DB	84	ETFGDDRTQVFAMATPEDLEANA	EYIRMA	DQYIEVPGGTNNNNYANVD	LI	VDIAERADV 143
QY	123	HAVWAGWGHASENPRLPESLAASKH	KIIFIGPPGSAMRSLGDKIS	S	TIVAQAHDVPCMPW 182	
DB	144	DAVWAGWGHASENPLLPKLSQSKR	KVIFIGPPGNAMRSLGDKIS	S	TIVAQAQAKVPCIPW 203	
QY	183	SGTGIKETMMSDQ--GFLT	VSDDVYQQACIHTAEEGLEKAE	KIGYPM	IKASEGGGKGI 240	
DB	204	SGTGV-DTVHVDEK	TGLVSDDIYQKGCCTSP	EDGLQAKRIGFP	PMIKASEGGGKGI 262	
QY	241	RKCTNGEEFKQLYNAV	LGEVPGSPVFMKLAGQARH	LEVQLLADQY	NAISIFGRDCSVQ 300	
DB	263	RQVEREEDFIALYHQ	AANEIPGSPIFIMKLAGR	ARHLEVQLLADQY	GTNISLFGDCSVQ 322	
QY	301	RRHQKIIIEAPVTI	APDARESMEKAAVR	LAKLVGYVSAGT	VEWLYSPESGEFAFLINP 360	
DB	323	RRHOKIIEAPVTIA	EKTTFHEMEKAAVR	LKLVGYVSAGT	VEYLYSHDDGKFYFLEINP 382	

QY	361	RLQVEHP	TTEMVSGVNIPAAQLQVAMGPIYSIRDITRTLYGMDPRGNEVIDFD	FSSPESF	420
Dd	383	RLQVEHP	TTEMVSGVNLPAALQIAMGIPMHRISDIRTYLGMNPHSASEIDFEFKTQDAT	442	
QY	421	KTOR	KPOQGHVVACRITAENPDGTGFKPGMGALTENFRSSTSTWGYFSVTSGALHEYA	480	
Dd	443	KKORR	PIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRRSSNVWGYSVGNNGNHSFS	502	
QY	481	DSQFGHIFAYGA	DSEARKQMVISLKELSI	RGDFTTVEYLKLETDAFESNKITTGWL	540
Dd	503	DSQFGHIFAFGEN	RQASRKHMVVALKELSI	RGDFTTVEYLKLETDATEDFNITTGWL	562
QY	541	DGLIQDRLTAERPPADLAV	559		
Dd	563	DDLITHKMATAEKPPDTI	LAV	581	

RESULT 3  
 US-08-354-973-1  
 ; Sequence 1, Application US/08354973  
 ; Patent No. 5641666  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vahlensieck, Hans-Friedrich  
 ; APPLICANT: Hinnen, Albert  
 ; TITLE OF INVENTION: Fungi Resistant to Soraphen A  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Ciba-Geigy Corporation  
 ; STREET: Patent Dept., 520 White Plains Rd., POB 2005  
 ; CITY: Tarrytown  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10591-9005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/354,973  
 ; FILING DATE: 13-DEC-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pace, Gary  
 ; REGISTRATION NUMBER: 40,403  
 ; REFERENCE/DOCKET NUMBER: PF/5-19802/A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919-541-8582  
 ; TELEFAX: 919-541-8689  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2237 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Protein  
 ; HYPOTHETICAL: NO  
 US-08-354-973-1

	Query Match	70.9%;	Score 2060;	DB 1;	Length 2237;
	Best Local Similarity	69.1%;	Pred. NO. 2.7e-179;		
	Matches 386;	Conservative	76;	Mismatches 89;	Indels 8; Gaps 3;
QY	3	PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAA VKEIRSRKWAY	62		
DB	29	PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAA VKEIRSVRKWAY	83		
QY	63	ETFGDERAIEFTVMATPEDLKVNADYIRNADQYVEVPGGSSNNNNYANVDLIVDVAERAGV	122		
DB	84	ETFGDDRTVQFVAMATPEDLEARNAEYIRNADQYIEVPGGTNNNNYANVDLIVDIAERADV	143		
QY	123	HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVP	182		



Db 144 DAVWAGWCHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVASAKVPCIPW 203  
QY 183 SGTGIKETMMSDQ--GFLTVDVDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240  
Db 204 SGTGV-DTVHVEKTLGLVSDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 262  
QY 241 RKCTNGEEFKQLYNALVEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 263 RQVEREEDFIALYHQANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGRDCSVQ 322  
QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEPAFLELNP 360  
Db 323 RRHQKIIIEAPVTIAKAETTFHEMEKAAVRLKLVGYVSAGTVEYLYSHDDGKPYFLELNP 382  
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420  
Db 383 RLQVEHPTTEMVSGVNLIPAAQLQIAMGIPMHRISIRDITLYGMNPHSASEIDPEFKTQDAT 442  
QY 421 KTORKPOQGHVVACRITAEENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 443 KKQRRPIPKGCHCTACRITSEDPNDGFKPSGGTLHELNFRSSNVWGYFSVGNNGNIHSFS 502  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 540  
Db 503 DSQFGHIFAFGENRQASRKGMVVALKELSIRGDFRTTVEYLIKLETTEDPEDNTITGWL 562  
QY 541 DGLIQDRLTAERPDPADLAV 559  
Db 563 DDLITHKMTAEKPDPTLAV 581

RESULT 4

US-09-433-043B-119  
; Sequence 119, Application US/09433043B  
; Patent No. 6399342

GENERAL INFORMATION:

; APPLICANT: HASELKORN, ROBERT  
; APPLICANT: GORNICKI, PIOTR  
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE  
; FILE REFERENCE: ARCD:338US  
; CURRENT APPLICATION NUMBER: US/09/433,043B  
; CURRENT FILING DATE: 1999-10-25  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/475,879  
; PRIOR FILING DATE: 1992-10-02  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 119  
; LENGTH: 853  
; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-433-043B-119

Query Match 61.2%; Score 1780; DB 2; Length 853;

Best Local Similarity 63.4%; Pred. No. 3e-154;

Matches 343; Conservative 81; Mismatches 103; Indels 14; Gaps 5;

QY 22 ASPVADFIRKQGGHSHVITKVLICNNGIAA VKEIRSIRKWAYETFGDERAIEFTVMATPED 81

Db 103 ASP-AEFVTRFGGNNRVIEKVLIANNGIAA VKCMRSIRRSYEMFRNERAIRFVVMVTPE 161

QY 82 LKVNADYIRMADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141

Db 162 LKANA EYIKMADHYVPVPGGNNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLP 221

QY 142 LAASKHKIIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGKETMMSD---QGFL 198

Db 222 L--HKNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWNGSLRVDWQENDLQKRIL 279

QY 199 TVSDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNALVG 258  
Db 280 NVPQELYEKGVYKDDADDGLRAAEVGVYPVMIKASEGGGKGIKRVNNAADFPNLFQVQA 339  
QY 259 EVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVTIAPED 318  
Db 340 EVPGSPIFVMRLAKQSRHLEVQILADQYGNALISLFGRDCSVQRRHQKIIIEAPASIATSV 399  
QY 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEPAFLELNPRLQVEHPTTEMVSGVNIP 378  
Db 400 VFEHMEQCAVKLAKWGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNL 458  
QY 379 AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTORKPQPOGHVVACRIT 438  
Db 459 AAQLQIAMGIPLHRIKDIRVMYGVSPWGDGSDIDFENSA-----HVPGRGHVIAARIT 511  
QY 439 AENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498  
Db 512 SENPDEGFKPSSGTVOELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSWGENREEAI 571  
QY 499 KQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLDGLIQDRLTAERPDPADLA 558  
Db 572 SNMVVALKELSIRGDFRTTVEYLIKLETTESFQONRIDTGWLDRLIAEKVQAERPDTMLG 631  
QY 559 V 559  
Db 632 V 632

RESULT 5

US-09-433-043B-118  
; Sequence 118, Application US/09433043B  
; Patent No. 6399342

GENERAL INFORMATION:

; APPLICANT: HASELKORN, ROBERT  
; APPLICANT: GORNICKI, PIOTR  
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE  
; FILE REFERENCE: ARCD:338US  
; CURRENT APPLICATION NUMBER: US/09/433,043B  
; CURRENT FILING DATE: 1999-10-25  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/475,879  
; PRIOR FILING DATE: 1992-10-02  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 118  
; LENGTH: 852  
; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-433-043B-118

Query Match 60.7%; Score 1765.5; DB 2; Length 852;

Best Local Similarity 63.3%; Pred. No. 6.5e-153;

Matches 343; Conservative 80; Mismatches 104; Indels 15; Gaps 6;

QY 22 ASPVADFIRKQGGHSHVITKVLICNNGIAA VKEIRSIRKWAYETFGDERAIEFTVMATPED 81

Db 102 ASP-AEFVTRFGGNNRVIEKVLIANNGIAA VKCMRSIRRSYEMFRNERAIRFVVMVTPE 160

QY 82 LKVNADYIR-MADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPE 140

Db 161 LKANA EYIKMADHYVPVPGGNNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPE 220

QY 141 SLAASKHKIIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGKETMMSD---QGF 197

Db 221 LLL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWNGSLRVDWQENDFSKRI 278

QY 198 LTVSDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNALV 257

```

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
279 LNVFQDLYEKGYVKDVGDLKAAEEVGYPMWIKASEGGGKGIRKVVNADFPNLFQVQ 338

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
258 GEVPGSPVFMKLAGQARHLEVOLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPE 317
| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
339 AEVPGSPIFVMRLAKQSRHLEVOLLADQYGNASISLGRDCSVQRRHQKIIIEEAPAAIATP 398

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
318 DARESMEKAAVRKLGVYVSAGTVEWLVSPESEGEFAFLELNPRQLQVEHPTTEMVSGVNI 377
| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
399 AVFEHMEQCAVKLAKMVGYVSAGTVEYLYS-QDGSFYFLELNPRQLQVEHBPCTEMVADVNL 457

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
378 PAAQLQVAMGIPLYSIRDITLYGMDPPRGNEVIDDFSSPESFKTQRKQPQGHVVAACRI 437
| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
458 PAAQLQIAMGIPLFRIKDIRMMYGVSPWGDAPIDFENSA-----HVPCPRGHVIAARI 510

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
438 TAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA 497

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
511 TSENPEGEKEKSPSGTVQELNFRSNKNVWGYFSVAAAAGGLHEFADSQFGHCFSWGENREEA 570

| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
498 RKQWYISLKELSIRGDFRTTVEYLIKLLTDAFESKNITTTGWLGDGLIQDRLTAERPPADL 557
| | | | | : : : | | : : | | | | | | | | | | | : : | | : |
571 ISNMVVALKELSIRGDFRTTVEYLIKLLTESFQLNRIIDTGWLDRLIAEKVQAEERPDTML 630

558 AV 559
631 GV 632

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RESULT 6  
 US-08-677-010-3  
 ; Sequence 3, Application US/08677010  
 ; Patent No. 5925805  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ohlrogge, John B.  
 ; APPLICANT: Roesler, Keith R.  
 ; APPLICANT: Shorrosh, Basil S.  
 ; - TITLE OF INVENTION: Structure and Expression of an  
 ; TITLE OF INVENTION: Arabidopsis Acetyl-coenzyme A Carboxylase Gene  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
 ; STREET: P.O. Box 828  
 ; CITY: Bloomfield Hills  
 ; STATE: Michigan  
 ; COUNTRY: U.S.A.  
 ; ZIP: 48303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/677,010  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, Deann F.  
 ; REGISTRATION NUMBER: 36683  
 ; REFERENCE/DOCKET NUMBER: 6550-00002CPA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810)641-1600  
 ; TELEFAX: (810)641-0270  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2254 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 US-08-677-010-3

Matches	301;	Conservative	97;	Mismatches	143;	Indels	24;	Gaps	5
QY	4	DKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAAVKIERSIRKWAYE	63						
Db	8	NHSAV-----GPGINYEYTSQVDEFCKALRGKRPIHSILIANNGMAAAVKFIRSVRTWAYE	62						
QY	64	TFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSSNNNNYANVDLIVDVAERAGVH	123						
Db	63	TFGTEKAILLVGMATPEDMRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEMAEVTRVD	122						
QY	124	AVWAGWGHASENPRLPESLAASKHKIIFIGPPGGSAMRSLGDKISSTIVAQAHDVPCMPWS	183						
Db	123	AVWPWGHASENPELPDALDAK--GIIFLPGPPASSMAALGDKIGSSLIAQAADVPTLPWS	180						
QY	184	GTGIKETWMSDQGFELTVSDDVYQOACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKC	243						
Db	181	GSHVK--IPPNSLVTIPEEIYRQACVYTTTEAIAASCQVVGVGPAMIKASWGGGKGIRKV	238						
QY	244	TNGEEFKQLYNALGVEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRH	303						
Db	239	HNDDEVRALEFKVQGEVPGSPIFIMKVASQSRHLEVQLLCDKHGNNVSALHSRDCSVQRRH	298						
QY	304	QKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQ	363						
Db	299	QKIIIEGPITVAPPETVKKLEQAARRLAKSVNYVGAATIEVLYSMDTGYYFFLELNPRLQ	358						
QY	364	VEHPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDITRTLYGMDPRGN-----EVIDFDF	414						
Db	359	VEHPVTEWIAEINLPAAQVAVGMGIPLWQIPEIRRFYGIHGGGYDSWRKTSVVAFFPFD	418						
QY	415	SSPESFKTORKPQOGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTWGYFVSGTSG	474						
Db	419	DKAQSIR-----PKGHCVAVRVTSEDDPDGFKPTSGRVQELSFKSKPNVWAYFVSKSGG	472						
QY	475	ALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLLETDAFESNK	534						
Db	473	GIHEFSDSQFGHVFAFGESRALAIANMVLGLKEIQIRGEIRTNVDYITIDLLHASDYRDNK	532						
QY	535	ITTGWLDDGLIQDRLTAERPPPADLAV	559						
Db	533	IHTGWLDSRIAMRVRAERPPPWYLSV	557						

RESULT 7  
US-08-790-519-3  
; Sequence 3, Application US/08790519  
; Patent No. 5962767  
; GENERAL INFORMATION:  
; APPLICANT: Ohlrogge, John B.  
; APPLICANT: Roesler, Keith R.  
; APPLICANT: Shorrosh, Basil S.  
; TITLE OF INVENTION: Structure and Expression of an  
; TITLE OF INVENTION: Arabidopsis Acetyl-coenzyme A Carboxylase Gene  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: Michigan  
; COUNTRY: U.S.A.  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/790,519  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/248,630  
; FILING DATE:





```

; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17027

Query Match      54.0%; Score 1569.5; DB 2; Length 442;
Best Local Similarity 70.2%; Pred. No. 2.3e-135;
Matches 295; Conservative 49; Mismatches 75; Indels 1; Gaps 1;

QY 101 GSNNNYANVDLIVDAERAGVHAWGCHASENPRLPESLAASKHIIIFGPPGSAMR 160
Db 14 GTNNNNYANVDLIVEIAESTNAHAWGCHASENPLLEKLAASPKKIIIFGPPGSAMR 73

QY 161 SLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQ-GFLTVDVYQQACIHTAEGLK 219
Db 74 SLGDKISSTIVAQAHAQVPCIPWSGTGVDEVKIDPQTNLVSADDIYAKGCCTSPEDGLEK 133

QY 220 AEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVLGEVPGSPVFVMKLAGQARHLEV 279
Db 134 AKKIGFPVMIKASEGGGKGIRKVDDEKNFITLYNQAAEIPGSPIFIMKLAGDARHLEV 193

QY 280 QLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSA 339
Db 194 QLLADQYGTNISLFRDCSVQRRHQKIIIEEAPVTIARKETFHEMENAAVRLKLVGYVSA 253

QY 340 GTVEWLYSPESGEFAFLELNPRLQVEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDRTL 399
Db 254 GTVEYLYSHAEDKFYFLELNPRLQVEHPPTTEMVTGVNLPAAQLQIAMGIPMRIRDRTL 313

QY 400 YGMDPRGNEVIDFESSPESFKTQKQPQGHVVACRITAENPDGTGFKPGMGALTELNFR 459
Db 314 YGADPHTTTDDIFEKSETSLVSQRRPTPKGHCTACRITSEDPEGEFKPSGSLHELNFR 373

QY 460 SSTSTWGYFSGVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVE 519
Db 374 SSSNVWGYFSGVGNQSSIHSPDSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVD 433

RESULT 10
US-08-611-107-10
; Sequence 10, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-611-107-10

Query Match      53.8%; Score 1565; DB 1; Length 2257;
Best Local Similarity 54.6%; Pred. No. 7.5e-134;
Matches 300; Conservative 91; Mismatches 132; Indels 26; Gaps 5;

QY 23 SPVADFIRKQGGHVSITKVLICNNGLIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDL 82
Db 12 SSVDEFCKALGDSPIHSLVYANNNGMAAVKFMRSIRTWALETFGNEKAILLVAMATPEDL 71

QY 83 KVNADYIRMAHQYVEVPVPGSSNNNNYANVDLIVDAERAGVHAWGCHASENPRLPESL 142
Db 72 RINAEHIRIADQFLEVPVGGTNNNNYANVQLIVEIAERTRVSAVWPGWCHASENPELPDAL 131

QY 143 AASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGIK---ETMMSDQGFILT 199
Db 132 --MEKGIIFLGPPSAAMGALGDKIGSSLIQAAGVPTLPWSGSHVKVPQETCHS----- 183

QY 200 VSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVLGE 259
Db 184 IPPEIYKNACVSTTDEAVASCQVVGYPAMIKASWGGGKGIRKVNDDDEVRLAFKQVQGE 243

QY 260 VPGSPFVMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDA 319
Db 244 VPGSPFIMKVASQSRHLEVQLLCKHGNVAALHSRDCSVQRRHQKIIIEEGPITVAPPET 303

QY 320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPPTTEMVSGVNI 379
Db 304 IKELEQAARRLAKVCYQQAATVEYLYSMETGEYFLELNPRLQVEHPVTEWIAEINLPA 363

QY 380 AOLQVAMGIPLYSIRDITLYGMDPRGN-----EVIDFESSPESFKTQKQPQ 430
Db 364 SQVWVGMIPLYNIPERIRFYGIEHGGYHAWKEISAVATKFDLDKAQSVK-----PKG 417

QY 431 HVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSGVGTSGALHEYADSQFGHIFAY 490
Db 418 HCVAVRTSEDDDDGFKPTSGRVEELNFKSKPNVWAYFYSKSGGAIHEFSDSQFGHVFAF 477

QY 491 GADRSEARKQMVISLKELSIRGDFRTTVEYLYKLLETDAFESNKITTCGLDGLIQRDLTA 550
Db 478 GESRSLAIANMVLGLKEIQIRGEIRTNVDYTVDLLNAAEYRENKIHTGWLDSRIAMRVRA 537

QY 551 ERPPADLAV 559
Db 538 ERPPWYLSV 546

RESULT 11
US-08-422-560A-10
; Sequence 10, Application US/08422560A
; Patent No. 5910626
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
```



Db 184 IPBIIYKNACVSTTDEAVASQVVGYPAMIKASWGGGKGIRKVNHDDEVRLPFKQVQGE 243  
QY 260 VPGSPVFMKLAGOARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDA 319  
Db 244 VPGSPIFIMKVASQSRHLEVQLLCKHGNVAALHSRDCSVQRRHQKIIIEGPITVAPPET 303  
QY 320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPA 379  
Db 304 IKELEQAARRLAKVCYQGAATVEYLYSMETGEYFYFLELNPRLQVEHPVTEWIAINLPA 363  
QY 380 AQLQVAMGIPLYSIIRDITLYGMDPRGN-----EVIDFDFSSPESFKTQKPPQ 430  
Db 364 SQVVVGMGIPLYNIPEIRRFYGIHGGGYHAWKEISAVATKFDLDKAQSVK-----PKG 417  
QY 431 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY 490  
Db 418 HCVAVRVTSEDPDDGFKPTSGRVEELNFKSKPNVWAYFSVKSGGAIHEFSDSQFGHVFAF 477  
QY 491 GADRSEARKQMVISLKELSIKELSGIRGDFRTTVEYLYKLLETDAFESNKITTCGLDGLIQDRLTA 550  
Db 478 GESRSLAIANMVLGLKEIQIRGEIRTNVDYTVDLLNAABYRENKIHTGWLDSRIAMRVRA 537  
QY 551 ERPPADLAV 559  
Db 538 ERPPWYLSV 546

RESULT 13  
US-08-934-386-9  
; Sequence 9, Application US/08934386  
; Patent No. 6306636  
; GENERAL INFORMATION:  
; APPLICANT: Haselkorn, Robert  
; APPLICANT: Gornicki, Piotr  
; TITLE OF INVENTION: Methods for Detecting Nucleic Acid  
; TITLE OF INVENTION: Segments Encoding Acetyl-CoA Carboxylase  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: US  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,386  
; FILING DATE: 19-SEP-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: ARSB:521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: one-of(291, 316, 335, 586, 587)  
; OTHER INFORMATION: /note= "Xaa = Any Amino Acid"

US-08-934-386-9 Query Match 53.2%; Score 1547.5; DB 2; Length 2311;

Best Local Similarity 53.5%; Pred. No. 3.1e-132;  
Matches 294; Conservative 95; Mismatches 140; Indels 21; Gaps 5;  
QY 20 APASPVADFIKQGGHVSITKVLICNNGIAAIVKEIRSIRKWAYETFGDERAIEFTVMATP 79  
Db 114 ASLSKVVEFCMALGGKTPIHSVLVANNGMAAAKFMRSVRTWANETFGSEKAIQLIAMATP 173  
QY 80 EDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLP 139  
Db 174 EDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVEIAVRTGVSAVWPGWGHASENP 233  
QY 140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWPGSGTGK---ETMMSDQ 196  
Db 234 DALNA--NGIVFLGPPSSSMNALGDKVGSALIAQAAGVPTLPWSGSQVEIPLEVCLD--- 288  
QY 197 FLTVSDDVYQOACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNCEEFKQLYNAV 256  
Db 289 --SIXAEMYRKACVSTTEALASCOMIGYXAMIKASWGGGKGIRKVNXXDDVRLFKQV 346  
QY 257 LGEVPGSPVFMKLAGOARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAP 316  
Db 347 QGEVPGSPIFIMRLASQSRHLEVQLLQDQYGNVAALHSRDCSVQRRHQKIIIEEGPVTVP 406  
QY 317 EDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVN 376  
Db 407 RETVKELEQAARRLAKAVGYVGAATVEYLYSMETGEYFYFLELNPRLQVEHPVTEWIAEVN 466  
QY 377 IPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFD-----FSSPESFKTQKPPQ 429  
Db 467 LPAAQVAVGMGIPLWQVPEIRRFYGMNDGGG----YDIWRKTAALATPFNDFEVDSDQWPK 522  
QY 430 GHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFA 489  
Db 523 GHCVAVRITSEDDDDGFKPTGGKVKKEISFKSKPNVWAYFSVKSGGGGHEFADSQFGHVFA 582  
QY 490 YGADRSEARKQMVISLKELSIKELSGIRGDFRTTVEYLYKLLETDAFESNKITTCGLDGLIQDRLT 549  
Db 583 YGVXAAAITNMSLALKEIQIRGEIHSNVDYTVDLLNASDFKENRHTGWLDRNRIAMRVQ 642  
QY 550 AERPPADLAV 559  
Db 643 AERPPWYISV 652

RESULT 14  
US-08-417-089-6  
; Sequence 6, Application US/08417089  
; Patent No. 6069298  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHODS AND AN ACETYL COA CARBOXYLASE GENE  
; TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN  
; TITLE OF INVENTION: OIL CONTENT OF PLANTS  
; NUMBER OF SEQUENCES: 11  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,089  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2325 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-417-089-6  
Query Match 53.1%; Score 1543.5; DB 2; Length 2325;  
Best Local Similarity 53.5%; Pred. No. 7.4e-132;  
Matches 294; Conservative 94; Mismatches 141; Indels 21; Gaps 5;



QY 20 APASPVADFIRKQGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP 79  
Db 114 ASVSKVVEFCAALGGKTPHISILVANNGMAAKFMRSVRTWANDTFGSEKAIQLIAMATP 173  
QY 80 EDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLP 139  
Db 174 EDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVGMAQKLGVSAVWPGWGHASENP 233  
QY 140 ESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPCMPWSGTGK---ETMMSDQ 196  
Db 234 DALTA--GIVFLGPPASSMNALGDKVGSALIAQAAGVPTLAWSGSHVEVPLECCLD-- 288  
QY 197 FLTVDSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEHEFKQLYN 256  
Db 289 --AIPEEMYRKACVTTTEEAASQVGVYPAMIKASWGGGKGIRKVNDDDEVRLFQ 346  
QY 257 LGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVT 316  
Db 347 QGEVPGSPIFVMRLASQSRHLEVQLLADQYGNVAALHSRDCSVQRRHQKIIIEGP 406  
QY 317 EDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMV 376  
Db 407 RETVKALEQAARRLAKAVGVGAATVEYLYSMETGDIYFLELNPRLQVEHPVTEW 466  
QY 377 IPAAQLQVAMGIPLYSIDRTLYGMDPRGNEVIDFD-----FSSPESFKTQKP 429  
Db 467 LPAAQVAVGMGIPLWQIPEIRRFYGMIDYGGG----YDIWRKTAALATPFNFDE 522  
QY 430 GHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFVSQVGTSGALHEYADSO 489  
Db 523 GHCVAVRITSEDDGDFKPTGGKVKKEISFKSKPNVWAYFSVKSGGGIHEFADSO 582  
QY 490 YGADRSEARKQMVISLKELSGIRGDFRTTVEYLIKLETDAFESNKITTGWL 549  
Db 583 YGLSRPAAITNMSLALKEIQIRGEIHSNVDYTVDLLNASDFRENKIHTGWL 642  
QY 550 AERPPADLAV 559  
Db 643 AERPPWYISV 652

RESULT 15  
US-08-695-651-6  
; Sequence 6, Application US/08695651  
; Patent No. 6146867  
; GENERAL INFORMATION:  
; APPLICANT: Gengenbach, B. G.  
; APPLICANT: Somers, D. A.  
; APPLICANT: Wyse, D. L.  
; APPLICANT: Gronwald, J. W.  
; APPLICANT: Egli, M. A.  
; APPLICANT: Lutz, S. M.  
; TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.  
; STREET: P.O. Box 2938  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,651  
; FILING DATE: 12-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/417089

; FILING DATE: 05-APR-1995  
; APPLICATION NUMBER: 08/014326  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 07/917462  
; FILING DATE: 21-JUL-1992  
; APPLICATION NUMBER: 07/538674  
; FILING DATE: 18-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 600.318US3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-373-6900  
; TELEFAX: 612-339-3061  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2325 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal  
; US-08-695-651-6

Query Match 53.1%; Score 1543.5; DB 2; Length 2325;  
Best Local Similarity 53.5%; Pred. No. 7.4e-132;  
Matches 294; Conservative 94; Mismatches 141; Indels 21; Gaps 5;  
QY 20 APASPVADFIRKQGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP 79  
Db 114 ASVSKVVEFCAALGGKTPHISILVANNGMAAKFMRSVRTWANDTFGSEKAIQLIAMATP 173  
QY 80 EDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLP 139  
Db 174 EDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVGMAQKLGVSAVWPGWGHASENP 233  
QY 140 ESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPCMPWSGTGK---ETMMSDQ 196  
Db 234 DALTA--GIVFLGPPASSMNALGDKVGSALIAQAAGVPTLAWSGSHVEVPLECCLD-- 288  
QY 197 FLTVDSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEHEFKQLYN 256  
Db 289 --AIPEEMYRKACVTTTEEAASQVGVYPAMIKASWGGGKGIRKVNDDDEVRLFQ 346  
QY 257 LGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVT 316  
Db 347 QGEVPGSPIFVMRLASQSRHLEVQLLADQYGNVAALHSRDCSVQRRHQKIIIEGP 406  
QY 317 EDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMV 376  
Db 407 RETVKALEQAARRLAKAVGVGAATVEYLYSMETGDIYFLELNPRLQVEHPVTEW 466  
QY 377 IPAAQLQVAMGIPLYSIDRTLYGMDPRGNEVIDFD-----FSSPESFKTQKP 429  
Db 467 LPAAQVAVGMGIPLWQIPEIRRFYGMIDYGGG----YDIWRKTAALATPFNFDE 522  
QY 430 GHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFVSQVGTSGALHEYADSO 489  
Db 523 GHCVAVRITSEDDGDFKPTGGKVKKEISFKSKPNVWAYFSVKSGGGIHEFADSO 582  
QY 490 YGADRSEARKQMVISLKELSGIRGDFRTTVEYLIKLETDAFESNKITTGWL 549  
Db 583 YGLSRPAAITNMSLALKEIQIRGEIHSNVDYTVDLLNASDFRENKIHTGWL 642  
QY 550 AERPPADLAV 559  
Db 643 AERPPWYISV 652

RESULT 16  
US-08-930-285-6  
; Sequence 6, Application US/08930285







US-08-418-893D-23  
; Sequence 23, Application US/08418893D  
; Patent No. 5559220  
; GENERAL INFORMATION:  
; APPLICANT: ROESSLER, PAUL G  
; APPLICANT: OHLROGGE, JOHN B  
; TITLE OF INVENTION: GENE THAT ENCODES ACETYL-COENZYME A  
; TITLE OF INVENTION: CARBOXYLASE FROM CYCLOTELLA CRYPTICA  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY  
; STREET: 1617 Cole Blvd.  
; CITY: Golden  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80401-3393  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/418,893D  
; FILING DATE: April 7, 1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/104,938  
; FILING DATE: September 14, 1993  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: O'CONNOR, EDNA  
; REGISTRATION NUMBER: 29,252  
; REFERENCE/DOCKET NUMBER: MRI/NREL IR# 92-48CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-231-1000  
; TELEFAX: 303-231-1098  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2089 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-418-893D-23  
Query Match 51.7%; Score 1502.5; DB 1; Length 2089;  
Best Local Similarity 53.2%; Pred. No. 3.6e-128;  
Matches 291; Conservative 95; Mismatches 140; Indels 21; Gaps 6;  
QY 22 ASPVADFIRKQGGHSHVITKVLICNNGLAAVKEIRSKWAVETFGDERAIEFTVMATPED 81  
Db 81 AKSVEDYVKSRGGRVIRKVLNNGMAATKSILSMQWAYMEFGDERAIOFVAMATPED 140  
QY 82 LKVNADYIRMADQYVEVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141  
Db 141 LKANAFFIRLADSFVEVPGGKLNLYANVDVITRIAEQGVDAVWPWGCHASENPKLPNA 200  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSITIVAQAHDVPCMPWSGT-----GIKETMMSDQ 195  
Db 201 L--DKLGKIFIGTGPVMSVLGDKIAANILAQTAKVPSIPWSGSGGPGDDPLQADLTEE 258  
QY 196 GFLTVDVYQQACIHTAEGLKAEKIGYP--VMIKASEGGGGKIRKCTNGEEFKQLY 253  
Db 259 G--TIPMEIFNKLGLVTSADAVIVANKIGWENGIMIKASEGGGGKIRFVDNEADLRNAP 316  
QY 254 NAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHQKIEEAPVT 313  
Db 317 VQVSNEVIGSPIFLMQLCKNARHIEVQIVGDQHGNAVALNCRDCSTORRFQKIFEEGPPS 376  
QY 314 IAPEDARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLELNPRQLQVEHPTTEMVS 373

Db 377 IVPKETHEMELAAQRLTQNGYQAGTVEYLYNAADNKKFFLELNPRQLQVEHPVTEGIT 436  
QY 374 GVNIPAAQLQVAMGIPLYSIRDITLYGM-DPRGNEVIDFDFSSPESFKTKRKPQGHV 432  
Db 437 GANLPATQLQVAMGIPLFNIPDIRRLYGREDAYGTDPID-----FLOERYRELDHSV 488  
QY 433 VACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGA 492  
Db 489 IAAARITAEENPDGFKPTSGSIERIKFQSTPNVWGYFSVGANGGTHEFADSQFGHLFAKGP 548  
QY 493 DRSEARKQMVISLKELSIKELSGDFTTVEYLYKLLETDAFESNKITTWGLDGLIQDRLTAER 552  
Db 549 NREQARKALVLALEMVREGDIRNSVEYLVKLETEAFKNTIDTSWLDGIIKEKSVKVE 608  
QY 553 PPADLAV 559  
Db 609 MPSHLVV 615  
RESULT 20  
US-08-418-893D-24  
; Sequence 24, Application US/08418893D  
; Patent No. 5559220  
; GENERAL INFORMATION:  
; APPLICANT: ROESSLER, PAUL G  
; APPLICANT: OHLROGGE, JOHN B  
; TITLE OF INVENTION: GENE THAT ENCODES ACETYL-COENZYME A  
; TITLE OF INVENTION: CARBOXYLASE FROM CYCLOTELLA CRYPTICA  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY  
; STREET: 1617 Cole Blvd.  
; CITY: Golden  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80401-3393  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/418,893D  
; FILING DATE: April 7, 1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/104,938  
; FILING DATE: September 14, 1993  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: O'CONNOR, EDNA  
; REGISTRATION NUMBER: 29,252  
; REFERENCE/DOCKET NUMBER: MRI/NREL IR# 92-48CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-231-1000  
; TELEFAX: 303-231-1098  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2089 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-418-893D-24  
Query Match 51.7%; Score 1502.5; DB 1; Length 2089;  
Best Local Similarity 53.2%; Pred. No. 3.6e-128;  
Matches 291; Conservative 95; Mismatches 140; Indels 21; Gaps 6;



```
; APPLICANT: MUL, ERNEST
; APPLICANT: MACK, DOUG
; APPLICANT: SAMUEL, BENJAMIN
; APPLICANT: GORNICKI, PIOTR
; APPLICANT: ZUTHER, ELLEN
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
; TITLE OF INVENTION: BASED ON UNIQUE APICOMPLEXAN PARASITE COMPONENTS
; FILE REFERENCE: 19338-90966
; CURRENT APPLICATION NUMBER: US/09/631,594
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US00/11478
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US97/12497
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-631-594-74
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Query Match 48.7%; Score 1417; DB 2; Length 489;
Best Local Similarity 55.2%; Pred. No. 2.7e-121;
Matches 277; Conservative 77; Mismatches 134; Indels 14; Gaps 5;
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Qy 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVP 99
Db 1 RVLIANNGMAATKSFISMRQWAYMELGDDKLLFVVMATPEDMRANPEFIRRADKIVEVP 60
Qy 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 61 GGNRRNNYANVDLICIAVQEKVDVAVWPGWGHASENPNLPRRL--SELGITFIGPSATVM 118
Qy 160 RSLGDKISSTIVAQHADVPCMPWSGTGIGKETMMSDQGFLTVDVDDVYQACIHTAEEGLEK 219
Db 119 AALGDKIAANILATAGVPSIPWSGDSLKATLDSTG--AIPRDFQATVKSVEECEKV 175
Qy 220 AEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEV 279
Db 176 ADRIGYPMIKASEGGGKGIRMDRKEQVRGAYEQVVAEVPGSPVFMQLCTAARHIEV 235
Qy 280 QLLADQYGNNAISIFGRDCSVQRRHQKIIIEA-PVTIAPEDARESMEKAAVRLAKLVGYVS 338
Db 236 QIVGDEGQAVALSGRDCSTQRRFQKIFEEAPPTTVVPPHTMKEMEKAQRLLTQSLGYVG 295
Qy 339 AGTVEWLYSPESGEFAFLELNPRQLQVEHPTTEMVSGWNIPAAQLQVAMGIPLYSIRDIRT 398
Db 296 AGTVEYLYNRKDDKFFFLFLELNPRQLQVEHPVSEGTGVNLPAAQLQVAMGIPLWRIPDIR 355
Qy 399 LYGMDPRGNEVIDFDSSPESFKTQKPOQGHVAVACRITAENPDTPGPKPMGALTENLF 458
Db 356 FFGDRPNAGDRI--DFINEDYLPQR-----HVLASRVTAENPDGPKPTSGRVDRLFE 407
Qy 459 RSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLSELSIRGDFRTTV 518
Db 408 QPLENVWGYFSVGASGVVHEYADSQFGHIFATGKNREARKKLVLGLKRVDRVGEIRTP 467
Qy 519 EYLKLETTDAFESNKITGWL 540
Db 468 EYLVQLLEDKDFIENRDTSWL 489
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RESULT 23
US-09-631-594-76
; Sequence 76, Application US/09631594
; Patent No. 6737237
; GENERAL INFORMATION:
; APPLICANT: MCLEOD, RIMA.W.
; APPLICANT: ROBERTS, CRAIG W.
; APPLICANT: ROBERTS, FIONA
; APPLICANT: JOHNSON, JENNIFER J.
; APPLICANT: KIRISITS, MICHAEL
```

```
; APPLICANT: FERGUSON, DAVID
; APPLICANT: LYONS, RUSSELL
; APPLICANT: MUI, ERNEST
; APPLICANT: MACK, DOUG
; APPLICANT: SAMUEL, BENJAMIN
; APPLICANT: GORNICKI, PIOTR
; APPLICANT: ZUTHER, ELLEN
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
; TITLE OF INVENTION: BASED ON UNIQUE APICOMPLEXAN PARASITE COMPONENTS
; FILE REFERENCE: 19338-90966
; CURRENT APPLICATION NUMBER: US/09/631,594
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US00/11478
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US97/12497
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-631-594-76
```

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Query Match 43.5%; Score 1265.5; DB 2; Length 506;
Best Local Similarity 49.5%; Pred. No. 2.3e-107;
Matches 263; Conservative 70; Mismatches 143; Indels 55; Gaps 6;
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Qy 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVP 99
Db 1 RLIANNGTAAVRCIRSMRWAYEALGNSKALEFVVMATAADIDANAEIFAEADFYVEVP 60
Qy 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 61 PGNSNNYANHLIVQTAETVECDVAVWPGWGHASENHRLPAILQTLKRKTWIGSPQAM 120
Qy 160 RSLGDKISSTIVAQHADVPCMPWSGT-----GIKETMMSDQ 195
Db 121 LALGDKIGSAVIAQSVNVPCVPWSGETRSPKRADTQPHSKTRRSISPPHFTRESM---- 176
Qy 196 GFLTVDVDDVYQACIHT-----ABEGLKAEKIGYPMIKASEGGGKGIRKCTNGEEFK 250
Db 177 -HLSISVSKVFLTCLWTHFAFLHQVLDCCAKIGYPMIKASEGGGKGIRRVTNAAEVA 235
Qy 251 QLYNAVLEVPVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEA 310
Db 236 DAYRQVNVNEVKGSPVFMVMSDCRHLLEVQLLADKSGRCVSLGSRDCSIQRRCKIIEEG 295
Qy 311 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRQLQVEHPTTE 370
Db 296 PVVAAPPEVVSQMEDAACRMAMAVGYENAGTCEFLYDPKTHQFAFLEVNARLQVEHVUTE 355
Qy 371 MVSGWNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDSSPESFKTQKPOQ 430
Db 356 CVGDFNLPAALQVAMGILIDDIPDIKA-----YLDASAASN-----KPVG 395
Qy 431 -HVVACRITAENPDTPGPKPMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFA 489
Db 396 KHIAARITAEHAEESFRPTVGLVHLELTFRPSRFVWGVFSIGSKGNIHAFNDAQFGHLFA 455
Qy 490 YGADRSEARKQMVISLSELSIRGDFRTTVEYLIKLETTDAFESNKITGWL 540
Db 456 HGKDRREAVKHMVLALKDMTIRGELRTNVEALIKILEHPDFVANETHHTWL 506
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RESULT 24
US-09-475-252-2
; Sequence 2, Application US/09475252
; Patent No. 6514726
; GENERAL INFORMATION:
; APPLICANT: Dorr, Patrick K.
; APPLICANT: Parkinson, Tanya
; APPLICANT: Bulawa, Christine Ellen
```



; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS ACETYL COENZYME-A CARBOXYLASE GENES
; TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 06286/107001
; CURRENT APPLICATION NUMBER: US/09/475,252
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/114,580
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2016
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-475-252-2

Query Match 39.6%; Score 1152; DB 2; Length 2016;
Best Local Similarity 75.2%; Pred. No. 5.2e-96;
Matches 221; Conservative 29; Mismatches 44; Indels 0; Gaps 0;

QY 266 FVMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEX 325
Db 2 FIMKLAGNARHLEVQLLADQYGNISLFGDCSVQRRHQKIIIEAPVTIAPATFQAMER 61

QY 326 AAVRLAKLVYVSAGTVEWLYSPESGEFAFLNPRQLQVEHPTTEMVSGVNIPAAQLQVA 385
Db 62 AAVSLGKLVYVSAGTVEYLYSHADDKFYFLNPRQLQVEHPTTEMVSGVNLPAALQIA 121

QY 386 MGIPLYSIRDIRTYLGMDPGRNEVIDFSSPESFKTORQPOQGHVVACRITAENPDG 445
Db 122 MGIPLHRIRDIRLYGVDPNTSSSEIDFSSPESFKTORRPOPKGHTTACRITSEDPGEG 181

QY 446 FKPGMGALTENFRSSTSTWGYFVSCTSGALHEYADSOFGHIFAYGADRSEARKQMVISL 505
Db 182 FKPSGGTMHLENFRSSNVWGYFVSCTAGGIHSFSDSQFGHIFAYGETRSASRKHMVVAL 241

QY 506 KELSIRGDFRTTVEYLIKLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
Db 242 KELSIRGDFRTTVEYLIKLETPAFEDNTITTGWLDQLISNKLTAERDPPIVAV 295

RESULT 25
US-07-956-700B-109
; Sequence 109, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 109:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474
; IDENTIFICATION METHOD: Xaa = any amino acid
US-07-956-700B-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

QY 227 VMKASEGGGKGIRKCTNGEFPKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQY 286
Db 1 VMKASWGGGKGIRKVNDDVRALFKQVQGEVPGSPFIMKVASQSRHLEVQLLCDKH 60

QY 287 GNAISIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEXAAVRLAKLVGYVSAGTVEWLY 346
Db 61 GNVAALHSRDCSVQRRHQKIIIEGPITVAPPETIKEQAARLAKVCVQYQGAATVEYLY 120

QY 347 SPESGEFAFLNPRQLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTYLGMDPGR 406
Db 121 SMETGEYFLELNPRLQVEHPTVEWIAEINLPASQVVVGMGIPLYNIPERRFYGIEHGG 180

QY 407 N-----EVIDFSSPESFKTORQPOQGHVVACRITAENPDGTFKPGMGALTEN 457
Db 181 GYHAWKEISAVATKFDLDKAQSVK-----PKGHCVAVRVTSDDPDGFKPTSGRVEELN 234

QY 458 FRSTSTWGYFVSCTSGALHEYADSOFGHIFAYGADRSEARKQMVISLKSIRGDFRTT 517
Db 235 FKSPNVWAYFSVXSGAIHEFSDSQFGHVFAVGESRSLAANMVLGLKEIQIRGEIRTN 294

QY 518 VEYLIKLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
Db 295 VDTVDDLNAEYREXNIHTGWLDSDRIAMRVRAERPPWYLSV 336

RESULT 26
US-08-476-537-109
; Sequence 109, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; FEATURE:  
; NAME/KEY: Xaa  
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474  
; IDENTIFICATION METHOD: Xaa = any amino acid  
US-08-476-537-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;  
Best Local Similarity 54.7%; Pred. No. 1.2e-79;  
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

QY 227 VMKASEGGGKIRKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQY 286  
Db 1 VMKASWGGGKIRKVHNDDEVRALEFKVQVGEVPGSPIFIMKVASQSRHLEVQLLCDKH 60  
QY 287 GNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLY 346  
Db 61 GNVAAALHSRDCSVQRRHQKIIIEEPIITVAPPETIKELEQAARLAKVCVYQGAATVEYLY 120  
QY 347 SPESGEFAFLELNPRQLQVEHPVTTEMVSGVNIIPAAQLQVAMGIPLYISIRDTLYGMDPRG 406  
Db 121 SMETGEYFFLELNPRQLQVEHPVTETWIAEINLPASQVVVGMGIPLYNIPEIRRFYGIEHGG 180  
QY 407 N-----EVIDDFSSPESFKTQKPOQGHVVACRITAENPDTPGKPGMGALTELN 457  
Db 181 GYHAWKEISAVATKFDLDKAQSVK-----PKGHCVAVRVTSEDDPDDGFKPTSGRVEELN 234  
QY 458 FRSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTT 517  
Db 235 FKSKPNVWAYFSVXSGGAIHEFSDSQFGHVFXGESRSLAIANMVLGLKEIQIRGEIRTN 294  
QY 518 VEYLKLETDAPESNKITTTGWLGLIQDRLTAERPPADLAV 559  
Db 295 VDYTVDLLNAAEYRENXIHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 27  
US-08-485-607-109  
; Sequence 109, Application US/08485607  
; Patent No. 5792827  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5792627th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,607  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/956,700  
; FILING DATE: 10/21/92

ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5792627thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; FEATURE:  
; NAME/KEY: Xaa  
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474  
; IDENTIFICATION METHOD: Xaa = any amino acid  
US-08-485-607-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;  
Best Local Similarity 54.7%; Pred. No. 1.2e-79;  
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

QY 227 VMKASEGGGKIRKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQY 286  
Db 1 VMKASWGGGKIRKVHNDDEVRALEFKVQVGEVPGSPIFIMKVASQSRHLEVQLLCDKH 60  
QY 287 GNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLY 346  
Db 61 GNVAAALHSRDCSVQRRHQKIIIEEPIITVAPPETIKELEQAARLAKVCVYQGAATVEYLY 120  
QY 347 SPESGEFAFLELNPRQLQVEHPVTTEMVSGVNIIPAAQLQVAMGIPLYISIRDTLYGMDPRG 406  
Db 121 SMETGEYFFLELNPRQLQVEHPVTETWIAEINLPASQVVVGMGIPLYNIPEIRRFYGIEHGG 180  
QY 407 N-----EVIDDFSSPESFKTQKPOQGHVVACRITAENPDTPGKPGMGALTELN 457  
Db 181 GYHAWKEISAVATKFDLDKAQSVK-----PKGHCVAVRVTSEDDPDDGFKPTSGRVEELN 234  
QY 458 FRSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTT 517  
Db 235 FKSKPNVWAYFSVXSGGAIHEFSDSQFGHVFXGESRSLAIANMVLGLKEIQIRGEIRTN 294  
QY 518 VEYLKLETDAPESNKITTTGWLGLIQDRLTAERPPADLAV 559  
Db 295 VDYTVDLLNAAEYRENXIHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 28  
US-08-475-879-109  
; Sequence 109, Application US/08475879  
; Patent No. 5972644  
; Patent No. 5972644 5786170  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5972644 5786170th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,879





QY 287 GNAISIFGRDCSVORRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLY 346  
Db 61 GNVAAALHSRDCSVORRHQKIIIEGPITVAPPETIKELEQAARRLAKVCYQGAATVEYLY 120  
QY 347 SPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYISIRDIRTLYGMDPRG 406  
Db 121 SMETGEYFLELNPRLQVEHPVTEWIAEINLPASQVVGMGIPLYINIPERRFYGIEHGG 180  
QY 407 N-----EVIDFESSPESFKTQKQPQGHVVACRITAENPDGTGFKPGMGALTELN 457  
Db 181 GYHAWKEISAVATKFDLDKAWSVK-----PKGHCVAVRVTSDEPDGDFKPTSGRVEELN 234  
QY 458 FRSSSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTT 517  
Db 235 FKSKPNVWAYFSVKGGAHEFSDSQFGHVFAFGESRSLAIANMVLGLKEIQIRGEIRTN 294  
QY 518 VEYLKLELDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559  
Db 295 VDYTVDLLNAAEYRENMHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 31  
US-08-611-107-6  
; Sequence 6, Application US/08611107  
; Patent No. 5801233  
; GENERAL INFORMATION:  
; APPLICANT: Haselkorn, Robert  
; APPLICANT: Gornicki, Piotr  
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING  
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES  
; TITLE OF INVENTION: THEREFOR  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,107  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US SN 07/956,700  
; FILING DATE: 02-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/US93/09340  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US SN 08/422,560  
; FILING DATE: 14-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: ARCD:221  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 447 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

US-08-611-107-6 Query Match 24.4%; Score 709.5; DB 1; Length 447;

Best Local Similarity 32.9%; Pred. No. 2.1e-56;  
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;  
QY 40 KVLICNNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMTATPEDLKNVADYIRMDQYVEVP 99  
Db 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53  
QY 100 GGSNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHKIIFIGPPGSAM 159  
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHIIAFIGPTPEAI 111  
QY 160 RSLGDKISSTIVAQHADVPCMPWSGTGKETMTMSDQGLTVSDVYQQACIHTAEEGLEK 219  
Db 112 RLMGDKSTAKETMQKAGVTPVPGS-----EGLVETEQEGLEL 148  
QY 220 AEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEV-----PGSPVFMKLAGQAR 275  
Db 149 AKDIGYPMIKATAGGGGRGMRVLVRSPDEFVKLFLAAQGEAGAAFGNAGVYIEKFIERPR 208  
QY 276 HLEVQLLADQYGNASIFGRDCSVORRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVG 335  
Db 209 HIEFQILADNYGNVIHLGERDCSIQRNQLLEAPSPALDSLDREKMGQAAVKAQFIN 268  
QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYISIRD 395  
Db 269 YTGAGTIEFLD-RSQQFYFMENVTRIQVEHPVTMTGVDLLVEQIRIAQGERLRLTQD 327  
QY 396 IRTLYGMDPRGNEVIDFDFSSPESFKTQKQPQGHVVACRITAENPDGTGFKPGMGALTE 455  
Db 328 QVVL-----RGHAIIECRINAEDPDHDFRPAPGRIS- 357  
QY 456 LNFRSSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGVRIDSHVYTDYQIPPYDLSLIGKLVGPDRTAATINRMKRA 407  
QY 505 LKELSIRGDFRTTVEYLKLELDAFESNKITTGWL 540  
Db 408 LRECAITG-LPTTIGFHQRI MENPQFLQGNVSTSFV 442

RESULT 32  
US-08-422-560A-6  
; Sequence 6, Application US/08422560A  
; Patent No. 5910626  
; GENERAL INFORMATION:  
; APPLICANT: Haselkorn, Robert  
; APPLICANT: Gornicki, Piotr  
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS FOR USE  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,560A  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/956,700  
; FILING DATE: 02-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:152/WIM

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-422-560A-6

Query Match      24.4%; Score 709.5; DB 1; Length 447;
Best Local Similarity 32.9%; Pred. No. 2.1e-56;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLVNADYIRMDQYVEVP 99
Db 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53

QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGTPEAI 111

QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLK 219
Db 112 RLMGDKSTAKETMQKAGVPTVPGS-----EGLVETEQEGLEL 148

QY 220 AEKIGYPVMIKASEGGGKIRKCTNGEEFKQLYNVAVLGEV----PGSPVFMKLAGQAR 275
Db 149 AKDIGYPVMIKATAGGGGRGMLVRSPDEFVKLFLAAQGEAGAAFGNAGVYIEKPIERPR 208

QY 276 HLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
Db 209 HIEFQILADNYGNVHILGERDCSIQRRNQKLLSEAPSPALDSDLREKMGQAAVKAQFIN 268

QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395
Db 269 YTGAGTIEFLLD-RSQGYFMEMNTRIQVEHPVTMTGVVDLLVEQIRIAQGERLRLTQD 327

QY 396 IRTLYGMDPRGNEVIDDFSSPESFKTQKPPQGHVHVACRITAENPDGTGFKPGMGALTE 455
Db 328 QVVL-----RGHAIECRINAEDPDHDFRPAAPGRIS- 357

QY 456 LNFIRSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504
Db 358 -----GYLPPGGPGVRIDSHVYTDYQIPPYVDSLIGKLIWGPDRATAINRMKRA 407

QY 505 LKELSIRGDFRTTVEYLKLETDAFESNKITTTGWL 540
Db 408 LRECAITG-LPTTIGFHQRIMENPQFLOQNVSTSFV 442
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RESULT 33
US-08-468-793-6
Sequence 6, Application US/08468793
Patent No. 6177267
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,560
FILING DATE: 14-APR-1995
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
CLASSIFICATION: 800
APPLICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-793-6
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Query Match      24.4%; Score 709.5; DB 2; Length 447;
Best Local Similarity 32.9%; Pred. No. 2.1e-56;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLVNADYIRMDQYVEVP 99
Db 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53

QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGTPEAI 111

QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLK 219
Db 112 RLMGDKSTAKETMQKAGVPTVPGS-----EGLVETEQEGLEL 148

QY 220 AEKIGYPVMIKASEGGGKIRKCTNGEEFKQLYNVAVLGEV----PGSPVFMKLAGQAR 275
Db 149 AKDIGYPVMIKATAGGGGRGMLVRSPDEFVKLFLAAQGEAGAAFGNAGVYIEKPIERPR 208

QY 276 HLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
Db 209 HIEFQILADNYGNVHILGERDCSIQRRNQKLLSEAPSPALDSDLREKMGQAAVKAQFIN 268

QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395
Db 269 YTGAGTIEFLLD-RSQGYFMEMNTRIQVEHPVTMTGVVDLLVEQIRIAQGERLRLTQD 327

QY 396 IRTLYGMDPRGNEVIDDFSSPESFKTQKPPQGHVHVACRITAENPDGTGFKPGMGALTE 455
Db 328 QVVL-----RGHAIECRINAEDPDHDFRPAAPGRIS- 357

QY 456 LNFIRSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504
Db 358 -----GYLPPGGPGVRIDSHVYTDYQIPPYVDSLIGKLIWGPDRATAINRMKRA 407

QY 505 LKELSIRGDFRTTVEYLKLETDAFESNKITTTGWL 540
Db 408 LRECAITG-LPTTIGFHQRIMENPQFLOQNVSTSFV 442

RESULT 34
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US-09-433-043B-122
; Sequence 122, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-122

Query Match      24.4%; Score 709.5; DB 2; Length 593;
Best Local Similarity 32.9%; Pred. No. 3.3e-56;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVP 99
Db 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53

QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGTPEAI 111

QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGLTVDVYQQACIHTAEGLVK 219
Db 112 RLMGDKSTAKETMQKAGVPTVPGS-----EGLVETELEGLEL 148

QY 220 AEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEV-----PGSPVFMKLAGQAR 275
Db 149 AKDIGYPMIKATAGGGGRGRLVRSDFEVKFLFLAAQGEAGAAFGNAGVIEKFIERPR 208

QY 276 HLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
Db 209 HIEFQILADNYGNVHILGERDCSIQRRNQKLLLEAPSPALDSDLREKMGQAAVKAAQFIN 268

QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVHEPTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395
Db 269 YAGAGTIEFLLD-RSGQFYFEMEMNTRIQVEHPVTMTVGTVDLLVEQIRIAQGERLRLTQD 327

QY 396 IRTLYGMDPRGNEVIDDFESSPESFKTQKPKQPGHVVACRITAENPDTGFKPGMGALTE 455
Db 328 QVVL-----RGHAIECRINAEDPDHDFRPAAPGRIS- 357

QY 456 LNFIRSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504
Db 358 -----GYLPPGGPGVRIDSHVYTDYQIPPYVDSLIGKLIWVGPDRATAINRMKRA 407

QY 505 LKELSIRGDFRTTVEYLKILETDAFESNKITTWGL 540
Db 408 LRECAITG-LPTTIGFHQRIEMENPQFLOQNVSTSFV 442
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RESULT 35

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US-08-611-107-8
; Sequence 8, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
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; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-611-107-8

Query Match      23.4%; Score 681.5; DB 1; Length 453;
Best Local Similarity 32.1%; Pred. No. 8e-54;
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVP 99
Db 5 KILIANRGEIALRILRACEELGIGTI-----AVHSTV-----DRNALHVQLADEAVCIG 53

QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EAASSKSYLNIPNIIAALTRNASAIHPGYGFLAENARFAEICA--DHHLTFIGPSPDSI 111

QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGLTVDVYQQACIHTAEGLVK 219
Db 112 RAMGDKSTAKETMQRVGVPTIPGS-----DGLLT--DV-----DSAAKV 148

QY 220 AEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEVP---GSP-VFVMKLAGQAR 275
Db 149 AAEIGYPMIKATAGGGGRGRLVREPADLEKLFLAAQGEAAAFNGPGLYLEKFIDRPR 208

QY 276 HLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
Db 209 HVEFQILADAYGNVVHILGERDCSIQRRHQKLLLEAPSPALSADLRQKMGDAARVKAQAIG 268

QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVHEPTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395
Db 269 YIGAGTVEFLVD-ATGNFYFEMEMNTRIQVEHPVTMTGLDLIAEQIRIAQG----- 319

QY 396 IRTLYGMDPRGNEVIDDFESSPESFKTQKPKQPGHVVACRITAENPDTGFKPGMGALTE 455
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Db 320 -----EALRF-----ROADIQLRGAIECRINAEDPEYNFRPNPGRIT- 357  
QY 456 LNFRSSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGVRVDSHVYTDYEIPPYDSLIGKLVWGATREAEIARMQRA 407  
QY 505 LKELSIRGDFRTTVEYLKLLTDAFESNKITTTGWLGLDGLIQDRL 548  
Db 408 LRECAITG-LPTTILSFHQLMQLMPFELRGELYTNFVEQVMLPRI 450  
RESULT 36  
US-08-422-560A-8  
; Sequence 8, Application US/08422560A  
; Patent No. 5910626  
; GENERAL INFORMATION:  
; APPLICANT: Haselkorn, Robert  
; APPLICANT: Gornicki, Piotr  
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS FOR USE  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,560A  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/956,700  
; FILING DATE: 02-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:152/WIM  
; TELEPHONE: 512-418-3000  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-422-560A-8  
Query Match 23.4%; Score 681.5; DB 1; Length 453;  
Best Local Similarity 32.1%; Pred. No. 8e-54;  
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;  
QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRNADQYVEVP 99  
Db 5 KILIANRGEIALRILRTCELGIGTI----AVHSIV-----DRNALHVQLADEAVCIG 53  
QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENRPDPESLAASKHKIIFIGPPGSAM 159  
Db 54 EAASSKSYLNIPNIIAALTRNASAIHPGYGFLAENARFAEICA--DHHLTFIGSPDSI 111  
QY 160 RSLGDKISSTIVAQHADVPCMPWSGTGKETMTMSDQGLTVSDVYQQACIHTAEGLEK 219  
Db 112 RAMGDKSTAKETMQRVGVPTIPGS-----DGLLT---DV-----DSAQKV 148  
QY 220 AEKIGYPMIKASEGGGKGIRKCTNGEETFQKLYNAVLEVP---GSP-VFVMKLAGQAR 275

Db 149 AAEGYPMIKATAGGGGRGRLVREPADLEKFLAAQGEAAAFGNPGLYLEKFIDRPR 208  
QY 276 HLEVQLLADQYGNNAISIFGRDCSVORRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVG 335  
Db 209 HVEFQILADAYGNVVHLGERDCSIQRHQLLEEAPSPALSADLRQKMGDAAVKVAQAIG 268  
QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395  
Db 269 YIGAGTVEFLVD-ATGNFYFMENTRIQVEHPVTEMITGLDLIAEQIRIAQG----- 319  
QY 396 IRTLYGMDPRGNEVIDDFESSPESFKTQKQPQGHVVACRITAENPDTCFKPGMGALTE 455  
Db 320 -----EALRF-----ROADIQLRGAIECRINAEDPEYNFRPNPGRIT- 357  
QY 456 LNFRSSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGVRVDSHVYTDYEIPPYDSLIGKLVWGATREAEIARMQRA 407  
QY 505 LKELSIRGDFRTTVEYLKLLTDAFESNKITTTGWLGLDGLIQDRL 548  
Db 408 LRECAITG-LPTTILSFHQLMQLMPFELRGELYTNFVEQVMLPRI 450  
RESULT 37  
US-08-468-793-8  
; Sequence 8, Application US/08468793  
; Patent No. 6177267  
; GENERAL INFORMATION:  
; APPLICANT: Haselkorn, Robert  
; APPLICANT: Gornicki, Piotr  
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,793  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/422,560  
; FILING DATE: 14-APR-1995  
; APPLICATION NUMBER: US SN 07/956,700  
; FILING DATE: 02-OCT-1992  
; CLASSIFICATION: 800  
; APPLICATION NUMBER: PCT/US93/09340  
; FILING DATE: 30-SEP-1993  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: ARCD:152/KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear



SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,537  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5756290thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-476-537-6

Query Match 23.4%; Score 679.5; DB 1; Length 453;  
Best Local Similarity 32.1%; Pred. No. 1.2e-53;  
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYVEVP 99  
Db 5 KILIANRGEIALRILRTCEELGIGTI---AVHSTV-----DRNALHVQLADEAVCIG 53  
QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGCHASENPRLPESLAASKHKIIFIGPPGSAM 159  
Db 54 EAASSKSYLNIPNIIAAALTRNASAIHPGYGFLAENARFAEICA--DHHLTFIGPSPDSI 111  
QY 160 RSLGDKISSTIVAQHADVPCMPWSGTGKETMMSDQGLFTVSDVYQQACIHTAEGLEK 219  
Db 112 RAMGDKSTAKETMQRVGVPTIPGS-----DGLLT---DV-----DSAAKV 148  
QY 220 AEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEVP---GSP-VFVMKLAGQAR 275  
Db 149 AAEIGYPVMIKATAGGGGRGMRVLVREPADLEKFLAAQGEAEAAFGNPGLYLEKFIIDRPR 208  
QY 276 HLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVG 335  
Db 209 HVEFQILADAYGNVVVELGERDCSIQRRHQKLEEAAPSALSADLRQKMGDAAVKVAQAIG 268  
QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPVTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395  
Db 269 YIGAGTVEFLVD-ATGNFYFMEWNTRIQVEHPVTTEMITGLDLIAEQIRIAQG-----319  
QY 396 IRTLYGMDPRGNEVIDFDFSSPESFKTQKPPQGHVAVACRITAENPDTCFKPGMGALTE 455  
Db 320 -----EALRP-----ROADIQLRGHAEICRINAEDPEYFNPNPGRIT- 357  
QY 456 LNFIRSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGRVVDVSHVYTDYEIPPYDSLIGKLIWVGATREAEIARMQRA 407  
QY 505 LKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGLDGLIQDRL 548  
Db 408 LREGAITG-LPTTLSFHQLMQMPEFLRGELYTNFVEQVWMLPRI 450

RESULT 40  
US-08-485-607-6  
; Sequence 6, Application US/08485607  
; Patent No. 5792627  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase

NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5792627th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,607  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5792627thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-485-607-6

Query Match 23.4%; Score 679.5; DB 1; Length 453;  
Best Local Similarity 32.1%; Pred. No. 1.2e-53;  
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMADQYVEVP 99  
Db 5 KILIANRGEIALRILRTCEELGIGTI---AVHSTV-----DRNALHVQLADEAVCIG 53  
QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGCHASENPRLPESLAASKHKIIFIGPPGSAM 159  
Db 54 EAASSKSYLNIPNIIAAALTRNASAIHPGYGFLAENARFAEICA--DHHLTFIGPSPDSI 111  
QY 160 RSLGDKISSTIVAQHADVPCMPWSGTGKETMMSDQGLFTVSDVYQQACIHTAEGLEK 219  
Db 112 RAMGDKSTAKETMQRVGVPTIPGS-----DGLLT---DV-----DSAAKV 148  
QY 220 AEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEVP---GSP-VFVMKLAGQAR 275  
Db 149 AAEIGYPVMIKATAGGGGRGMRVLVREPADLEKFLAAQGEAEAAFGNPGLYLEKFIIDRPR 208  
QY 276 HLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVG 335  
Db 209 HVEFQILADAYGNVVVELGERDCSIQRRHQKLEEAAPSALSADLRQKMGDAAVKVAQAIG 268  
QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPVTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395  
Db 269 YIGAGTVEFLVD-ATGNFYFMEWNTRIQVEHPVTTEMITGLDLIAEQIRIAQG-----319  
QY 396 IRTLYGMDPRGNEVIDFDFSSPESFKTQKPPQGHVAVACRITAENPDTCFKPGMGALTE 455  
Db 320 -----EALRP-----ROADIQLRGHAEICRINAEDPEYFNPNPGRIT- 357  
QY 456 LNFIRSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 358 -----GYLPPGGPGRVVDVSHVYTDYEIPPYDSLIGKLIWVGATREAEIARMQRA 407  
QY 505 LKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGLDGLIQDRL 548



Db 408 LREGAITG-LPTTILSFHQLMLQMPEFLRGELYTNEVEQVMLPRI 450

Search completed: February 4, 2006, 18:14:38  
Job time : 55 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:05:17 ; Search time 248 Seconds  
(without alignments)  
1590.284 Million cell updates/sec

Title: US-10-633-835-2  
Perfect score: 2907  
Sequence: 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDRLTAERPPADLAV 559

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	2907	100.0	2185	2 Q4P5I4_USTMA	Q4p5i4 ustilago ma
2	2896	99.6	2185	2 Q12721_USTMA	Q12721 ustilago ma
3	2269	78.1	2237	2 Q5KFC9_CRYNE	Q5kfc9 cryptococcu
4	2269	78.1	2237	2 Q55QT6_CRYNE	Q55qt6 cryptococcu
5	2190	75.3	2288	2 Q60033_EMENI	Q60033 emericella
6	2190	75.3	2288	2 Q5B004_EMENI	Q5b004 aspergillus
7	2186	75.2	2292	2 Q4X1V2_ASPFU	Q4xlv2 aspergillus
8	2179	75.0	2275	2 Q7SBL5_NEUCR	Q7sbl5 neurospora
9	2163	74.4	2344	2 Q51YC2_MAGGR	Q5lyc2 magnaporthe
10	2148	73.9	2271	2 Q4I878_GIBZE	Q4i878 gibberella
11	2100.5	72.3	2231	2 Q6CL34_KLULA	Q6cl34 kluyveromyc
12	2090.5	71.9	2233	2 Q6FKK8_CANGA	Q6fkk8 candida gla
13	2090.5	71.9	2280	1 COAC_SCHPO	P78820 schizosacch
14	2084	71.7	2266	2 Q6CC91_YARLI	Q6cc91 yarrowia li
15	2069.5	71.2	2231	2 Q75EK8_ASHGO	Q75ek8 ashbya goss
16	2061.5	70.9	2271	2 Q5AAM4_CANAL	Q5aam4 candida alb
17	2060	70.9	2233	1 COAC_YEAST	Q00955 saccharomyc
18	2039.5	70.2	2297	2 Q6BX58_DEBHA	Q6bx58 debaryomyc
19	1889.5	65.0	2273	1 HPA1_YEAST	P32874 saccharomyc
20	1889.5	65.0	2273	2 Q42823_YEAST	O42823 saccharomyc
21	1791	61.6	2346	2 Q6XDA8_HUMAN	Q6xda8 homo sapien
22	1787	61.5	2346	2 Q7Z561_HUMAN	Q7z561 rattus sapien
23	1785	61.4	2345	1 COA1_RAT	P11497 rattus norv
24	1783.5	61.4	2448	2 Q6JIZ0_MOUSE	Q6jiz0 mus musculu
25	1783	61.3	2345	2 Q5SWU9_MOUSE	Q5swu9 mus musculu
26	1781	61.3	2346	1 COA1_HUMAN	Q13085 homo sapien
27	1780	61.2	2323	2 Q9V346_DROME	Q9v346 drosophila
28	1780	61.2	2324	1 COAC_CHICK	P11029 gallus gall
29	1780	61.2	2482	2 Q9V347_DROME	Q9v347 drosophila
30	1776	61.1	2345	2 Q6JIZ1_MOUSE	Q6jiz1 mus musculu
31	1775	61.1	2346	1 COA1_BOVIN	Q9ttts3 bos taurus

RESULT 1					
Q4P5I4_USTMA					
ID	Q4P5I4_USTMA	PRELIMINARY;	PRT;	2185	AA.
AC	Q4P5I4;				
DT	13-SEP-2005	(TRENBLrel. 31, Created)			
DT	13-SEP-2005	(TRENBLrel. 31, Last sequence update)			
DT	13-SEP-2005	(TRENBLrel. 31, Last annotation update)			
DE	Hypothetical protein.				
GN	ORFNames=UM04629.1;				
OS	Ustilago maydis 521.				
OC	Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;				
OC	Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.				
OX	NCBI_TaxID=237631;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=521;				
RA	Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,				
RA	Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,				
RA	Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,				
RA	Bayul T., Blitshateyn B., Bloom T., Blye J., Boguslavskiy L.,				
RA	Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,				
RA	Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,				
RA	Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,				
RA	David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,				
RA	Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,				
RA	Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,				
RA	Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,				
RA	Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,				
RA	Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,				
RA	Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,				
RA	Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,				
RA	Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,				
RA	Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,				
RA	Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,				
RA	Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,				
RA	Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,				
RA	McCarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,				
RA	Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,				
RA	Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,				
RA	Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,				
RA	Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,				
RA	O'Neill K., Osman S., Parker S., Perin D., Phunkhang P., Piquani B.,				
RA	Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,				
RA	Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,				
RA	Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,				
RA	Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,				
RA	Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,				
RA	Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,				
RA	Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,				
RA	Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,				
RA	Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,				
RA	Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,				
RA	Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,				
RA	Zimmer A., Zody M., Lander E.;				

ALIGNMENTS

RT	"The genome sequence of Ustilago maydis.";									
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBDJ databases.									
CC	-!- CAUTION: The sequence shown here is derived from an									
CC	EMBL/GenBank/DBDJ whole genome shotgun (WGS) entry which is									
CC	preliminary data.									
DR	EMBL; AACP01000168; EAK85486.1; -; Genomic_DNA.									
KW	Hypothetical protein.									
SQ	SEQUENCE	2185	AA;	240063	MW;	8C2ECBF613483DF7	CRC64;			
	Query Match	100.0%;	Score	2907;	DB	2;	Length	2185;		
	Best Local Similarity	100.0%;	Pred. No.	2.9e-189;						
	Matches	559;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	PPPDHKAVSQFIGGNPLETAPASPVPADFIRKQGGHSHVITKVLICNNGIAA	KEIRSIRKW	60						
Db	2	PPPDHKAVSQFIGGNPLETAPASPVPADFIRKQGGHSHVITKVLICNNGIAA	KEIRSIRKW	61						
QY	61	AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGSSNNNNYANVDLI	VDVAERA	120						
Db	62	AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGSSNNNNYANVDLI	VDVAERA	121						
QY	121	GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVA	QHADVPCM	180						
Db	122	GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVA	QHADVPCM	181						
QY	181	PWSGTGIKETMSDQGLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASE	GGGGKGI	240						
Db	182	PWSGTGIKETMSDQGLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASE	GGGGKGI	241						
QY	241	RKCTNGEEFKOLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGN AISI	FGRDCSVQ	300						
Db	242	RKCTNGEEFKOLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGN AISI	FGRDCSVQ	301						
QY	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMWLYSPES	GEFAFLELNP	360						
Db	302	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMWLYSPES	GEFAFLELNP	361						
QY	361	RLQVEHPTTEMVSGVNI PAAQLQVAMGIPLY SIRDITLYGMDPRGNEVIDF	DSSPESF	420						
Db	362	RLQVEHPTTEMVSGVNI PAAQLQVAMGIPLY SIRDITLYGMDPRGNEVIDF	DSSPESF	421						
QY	421	KTQRKPOQGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTGWYFSVGT	SGALHEYA	480						
Db	422	KTQRKPOQGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTGWYFSVGT	SGALHEYA	481						
QY	481	DSQFGHIFAYGADRSEARKQMVISLKELSI RGDFTTVEYLIKLETDAFESN	KITTGWL	540						
Db	482	DSQFGHIFAYGADRSEARKQMVISLKELSI RGDFTTVEYLIKLETDAFESN	KITTGWL	541						
QY	541	DGLIQDRLTAERPPADLAV	559							
Db	542	DGLIQDRLTAERPPADLAV	560							

RT growth in *Ustilago maydis*.";  
RL Mol. Gen. Genet. 249:191-201(1995).  
DR EMBL; Z46886; CAA86983.1; -; Genomic\_DNA.  
DR PIR; S60200; S60200.  
DR HSP; Q00955; IOD4.  
DR SMR; Q12721; 11-545.  
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0009374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin BS.  
DR InterPro; IPR005482; Biotin\_carb C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPase\_L\_chain; 1.  
DR Pfam; PF02786; CPase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP\_GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; UNKNOWN\_1.  
DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS50989; COA\_CT\_CTER; 1.  
DR PROSITE; PS50980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPASE\_1; 1.  
DR PROSITE; PS00867; CPASE\_2; UNKNOWN\_1.  
KW Ligase.  
SQ SEQUENCE 2185 AA; 240031 MW; DDCEB709DBF8EFA9 CRC664

Barley A.M., Keen U.F.R., Owen U., Hargreaves U.A.;  
"The ACC1 gene, encoding acetyl-CoA carboxylase, is essential for





DR EMBL; AA001000031; EAL20176.1; -; Genomic\_DNA.  
DR SMR; Q55QT6; 24-557.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0009374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoYL.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoYL; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS00975; ATP\_GRASP; 1.  
DR PROSITE; PS00979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; UNKNOWN\_1.  
DR PROSITE; PS00968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS00989; COA\_CT\_CTER; 1.  
DR PROSITE; PS00980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 2237 AA; 248325 MW; A99AF395A7CA2E8E CRC64;

Query Match 78.1%; Score 2269; DB 2; Length 2237;  
Best Local Similarity 77.2%; Pred. No. 1.2e-145;  
Matches 429; Conservative 51; Mismatches 74; Indels 2; Gaps 1;  
  
QY 4 DHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAVKEIRSIRKWAYE 63  
DB 19 DHSKVAQFIGANSVESAPSGRVTDFVKAHNGHTVITKVLIANNGIAAVKEIRSIRKWSYE 78  
  
QY 64 TFGDERAIEFTVMATPEDLKNVADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH 123  
DB 79 TFGSDRQIEFTVMATPEDLRINAEYIRMADRYVEVPGGSNNNNYANVDLIVDVAERAGVH 138  
  
QY 124 AVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWS 183  
DB 139 AVWAGWGHASENPRLPETLA--KSKIIFIGPPGSAMRSLGDKISSTIVAQAHAQVPCMPWS 196  
  
QY 184 GTGIKETMMSDQGLTVDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKC 243  
DB 197 GTGISDTILSPQGFVTVPDKAYDDACVHSWEGLERAEEKIGFIPIMIKASEGGGKGIRKV 256  
  
QY 244 TNGEEFKQLYNALVEVPGSPVFMKLAGARHLEVQLLADQYGNNAISIFGRDCSVORRH 303  
DB 257 EDGEKFKNSFQAVAGEVPGSPIFMKLAGSARHLEVQLIADQYGNNAISLFGDRDCSVORRH 316  
  
QY 304 QKIIEEAPVTIAPEDARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLELNPRLQ 363  
DB 317 QKIIEEAPVTIAKPETFEEMEKAADVRLAKLVGVVSAGTVEYLYSHSDDSFYFLELNPRLQ 376  
  
QY 364 VEHPPTTMVSGVNIIPAAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVDIDFSSPESFKTQ 423  
DB 377 VEHPPTTMVSGCNIPAVQLQIAMGIPLHRIDRTLYGMDPHGITEIDFDGSKPESVNTQ 436  
  
QY 424 RKPOQGHVACRITAENPDGTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQ 483  
DB 437 RKPTPKGHVIACRITGENPDAGFKPSSGNLTTELNFRSNSNVWGYFSVSSAGGLHEYADSQ 496  
  
QY 484 FGHIFAYGADRSEARKQMVISLKELSIKSGDPRFTTVEYLIKLETDAPESNKITTTGLDGL 543  
DB 497 FGHIFAYGMESEARKSMVALKELSIKSGRFTTVEYLIKLEKPEFENNTLTQWL DGL 556  
  
QY 544 IQDRLTAERPADLAV 559

Db 557 IAEGMTSERPDPVVAV 572  
  
RESULT 5  
O60033 EMENI  
ID O60033 EMENI PRELIMINARY; PRT; 2288 AA.  
AC O60033;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Acetyl-CoA carboxylase (EC 6.4.1.2).  
GN Name=acca;  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=162425;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FGSC A26;  
RX MEDLINE=99087906; PubMed=9871120; DOI=10.1007/s002940050410;  
RA Morrice J., Mackenzie D.A., Parr A.J., Archer D.B.;  
RT "Isolation and characterisation of the acetyl-CoA carboxylase gene  
from Aspergillus nidulans.";  
RL Curr. Genet. 34:379-385(1998).  
DR EMBL; Y15996; CAA75926.1; -; Genomic\_DNA.  
DR PIR; T30568; T30568.  
DR HSSP; Q00955; 1OD4.  
DR SMR; O60033; 21-558.  
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0009374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoYL.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoYL; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS00975; ATP\_GRASP; 1.  
DR PROSITE; PS00979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS00968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS00989; COA\_CT\_CTER; 1.  
DR PROSITE; PS00980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
KW Ligase.  
SQ SEQUENCE 2288 AA; 255182 MW; 927E2518811EB1AB CRC64;

Query Match 75.3%; Score 2190; DB 2; Length 2288;  
Best Local Similarity 74.8%; Pred. No. 3.1e-140;  
Matches 415; Conservative 53; Mismatches 87; Indels 0; Gaps 0;

QY 5 HKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAVKEIRSIRKWAYE 64  
DB 19 HNLPSHFIGGNHLDAAAPSSVKDFVANHEGHSVITSLIANNNGIAAVKEIRSIRKWAYE 78  
  
QY 65 FGDERAIEFTVMATPEDLKNVADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124  
DB 79 FGNERAIQFTVMATPEDLAANADYIRMADQYVEVPGGTNNNNYANVELIVDVAERMDVHA 138  
  
QY 125 VWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSG 184





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Db 559 SNKLTAEPRDPTTIAV 573
RESULT 7
Q4X1V2_ASPFU
ID Q4X1V2_ASPFU PRELIMINARY; PRT; 2292 AA.
AC Q4X1V2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Acetyl-CoA carboxylase.
GN ORFNames=Afu2g08670;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majeros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalba M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000001; EAL93163.1; -; Genomic DNA.
SQ SEQUENCE 2292 AA; 254941 MW; 21624CBC5FBA7ED8 CRC64;

Query Match 75.2%; Score 2186; DB 2; Length 2292;
Best Local Similarity 74.2%; Pred. No. 5.9e-140;
Matches 412; Conservative 58; Mismatches 85; Indels 0; Gaps 0;

QY 5 HKAVSQFIGGNPLETAPSPVADPIRKQGHSHVITKVLICNNGIAAIVKEIRSKWAYET 64
Db 20 HNLPSHFIFGNGHLDAAAPSSVKDFVASHEGSHSVSSVLIANNNGIAAIVKEIRSKWAYET 79
QY 65 FGDERAIEFTVMTATPEDLKNVADYIRMDQYVEVPVGGSNNNNYANVDLIVDAERAGVHA 124
Db 80 FGNERAIQFTVMTATPEDLKNVADYIRMDQYVEVPVGGSNNNNYANVDLIVDAERAGVHA 139
QY 125 VWAGWGHASENPRLPESLAASKHIIIFIGPPGSMRSLGDKISSTIVAQHADVPICMPWSG 184
Db 140 VWAGWGHASENPRLPESLAASKHIIIFIGPPGSMRSLGDKISSTIVAQHADVPICMPWSG 199
QY 185 TGIKETMDSQGLFIVSDVYQACIHTAEGLKAPKIGYVPMIKASEGGGKGIRKCT 244
Db 200 TGVDEVTIDENGIVTPDEIYKRGCTFSPEEGLKKAKEIGFPMVKASEGGGKGIRKVE 259
QY 245 NGEFFKQLYNVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQ 304
Db 260 REEDFISLYNAAAANEIPGSPFIMKLAGNARHLEVQLLADQYGNISLFGDCSVQRRHQ 319
QY 305 KIIEEAPVTIAPEDARESMEKAARLAKLVGVYSAGTVWEWLYSPESGEFAFLELNPRLOV 364
Db 305 KIIEEAPVTIAPEDARESMEKAARLAKLVGVYSAGTVWEWLYSPESGEFAFLELNPRLOV 364
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Db 320 KIIEEAPVTIAPATFOAMERAAVSLGLVGVYSAGTVVEYLYSHADKFELELNPRLOV 379
QY 365 EHPTTEMVSGVNIIPAAQLOVAMGIPLYISIRDIRTLGYMDPRGNEVIDFSSPESFKTOR 424
Db 380 EHPTTEMVSGVNIIPAAQLOVAMGIPLYISIRDIRTLGYMDPRGNEVIDFSSPESFKTOR 439
QY 425 KPQPGHVACRITAENPDGFKPGMGALTELNFRRSSTSTWGYFSGTSGALHEYADSOF 484
Db 440 RPQPKGHTTACRITSEDGEGFKPSSGTMHNLFRSSNVWGYFSGTAGGIHSFSDSOF 499
QY 485 GHIFAYGADRSEARKQMVISLKELSGIRGDFRTTVEYLYKLLETFDAFESNKITTTGWL DGLI 544
Db 500 GHIFAYGENRSASRKGMMVVALKELSGIRGDFRTTVEYLYKLLETFDAFEDNTTTGWL DOLI 559
QY 545 QDRLTAERPPADLAV 559
Db 560 SNKLTAEPRDPIVAV 574

RESULT 8
Q7SBL5_NEUCR
ID Q7SBL5_NEUCR PRELIMINARY; PRT; 2275 AA.
AC Q7SBL5;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU08535.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000166; EAA33781.1; -; Genomic DNA.
DR HSSP; P24182; 1DV1.
DR SMR; Q7SBL5; 14-558.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR011763; COA_CT_C.
DR InterPro; IPR011762; COA_CT_N.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR005479; CPase_D2_ATP_bd.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
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Db 158 VWAGWGHAENPKLPESLAASPKKIIFIGPPGSAMRSLGDKISSITVAQHAQVPCIPWSG 217  
QY 185 TGIKETMMSDQGLTVSDDDVYQQACIHTAEGLKAEKIGYPMIKASEGGGKGIRKCT 244  
Db 218 TGVDVAVQIDKKGIVTVDDDTYAKGCVTSWQEGLEKARQIGFPMIKASEGGGKGIRKAV 277  
QY 245 NGEFEKQLYNVLGEVPGSPVFMVLMKLAGQARHLEVQLLADQYGNALISFGRDCSVQRRHQ 304  
Db 278 SEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNALISFGRDCSVQRRHQ 337  
QY 305 KIIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364  
Db 338 KIIEEAPVTIAKPDTEFKAMEEAAVRLGLVGYVSAGTVEYLYSHADDDKFFYLELNPRLQV 397  
QY 365 EHPTTEMVSGVNIAPAAQLQVAMGIPLYISIRDIRTYLGMPPRGNEVIDFSSPESFKTQR 424  
Db 398 EHPTTEGVSGVNLPAQLQIAMGIPLHRISDIRLLYGVDPKLSIDEIDFKNPDSEKTQR 457  
QY 425 KPQPOQHVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484  
Db 458 RPSPKGHLTACRITSEDPGEGFKPSNGVMHLELNFSSNVWGYFSVGTGGIHSFSDSQF 517  
QY 485 GHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTTGWLGLI 544  
Db 518 GHIFAYGENRSASRKHVMVIALKELSIKIRGDFRTTVEYLIKLETEAFEDNTISTGWLDELI 577  
QY 545 QDRLTAERPPADLAV 559  
Db 578 SKGLTAERPDKMLAV 592

RESULT 10

Q4I878 GIBZE  
ID Q4I878\_GIBZE PRELIMINARY; PRT; 2271 AA.  
AC Q4I878;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=FG06580.1;  
OS Gibberella zae PH-1.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
OX NCBI\_TaxID=229533;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PH-1;  
RA Birren B., Nisbaum C., Abouelleil A., Allen N., Anderson S.,  
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,  
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,  
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,  
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Illiev I.,  
RA Jaife D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,  
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,  
RA Mihova T., Mlenga V., Murphy T., Naylor T., Nguyen C., Nicol R.,  
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,  
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
RA Lander E.;

RT "Fusarium graminearum genome sequence."  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.  
DR EMBL; AACM01000259; EAA78365.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 2271 AA; 254510 MW; EC40D82850B76583 CRC64;  
Query Match 73.9%; Score 2148; DB 2; Length 2271;  
Best Local Similarity 72.4%; Pred. No. 2.3e-137;  
Matches 403; Conservative 64; Mismatches 90; Indels 0; Gaps 0;  
QY 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKESIRKWAY 62  
Db 18 PYFNIAHDFIGGNRLANAPSGKVKDFVAQNDGHTVITNVLIANNGIAAIVKESIRKWAY 77  
QY 63 ETPGDERAIEFTVMTATPEDLVNADYIRMDADQYVEVPGSSNNNNYANVDLIVDAERAGV 122  
Db 78 ETPRDERAIHFTVMTATPEDLQANAIEYIRMDADHYVEVPGGTNNNNYANVELIVDAERMV 137  
QY 123 HAVWAGWGHAENPKLPESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPMPW 182  
Db 138 HAVWAGWGHAENPKLPESLAASPNKIVFIGPPGSAMRSLGDKISSITVAQHAAPVPCIPW 197  
QY 183 SGTGIKETMMSDQGLTVSDDDVYQQACIHTAEGLKAEKIGYPMIKASEGGGKGIRK 242  
Db 198 SGTGVDQVAVDDKGIQVTVADDTYAGCVTSWEEGLEKAEKIGYPMIKASEGGGKGIRK 257  
QY 243 CTNGEEFKQLYNVLGEVPGSPVFMVLMKLAGQARHLEVQLLADQYGNALISFGRDCSVQRR 302  
Db 258 ATEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNALISFGRDCSVQRR 317  
QY 303 HQKIIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRL 362  
Db 318 HQKIIEEAPVTIAKPDTEFKAMEEAAVRLGLVGYVSAGTVEYLYSHDDEKFFYLELNPRL 377  
QY 363 QVEHPTTEMVSGVNIAPAAQLQVAMGIPLYISIRDIRTYLGMPPRGNEVIDFSSPESFXT 422  
Db 378 QVEHPTTEMVSGVNLPAQLQIAMGIPLHRIRDIRLLYGVDPKTSDDIDFEFKSEDTSSS 437  
QY 423 QRKPOQHVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADS 482  
Db 438 QRRPQPKGHTTACRITSEDPGEGFKPSNGVMHLELNFSSNVWGYFSVSSQGGIHSFSDS 497  
QY 483 QFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTTGWLGD 542  
Db 498 QFGHIFAYGENRSASRKHVMVIALKELSIKIRGDFRTTIEYLIKLETEAFEDNTISTGWLDE 557  
QY 543 LIQDRLTAERPPADLAV 559  
Db 558 LISKRLTAERPETMLAV 574

RESULT 11

Q6CL34 KLULA  
ID Q6CL34\_KLULA PRELIMINARY; PRT; 2231 AA.  
AC Q6CL34;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sp|Q00955 Saccharomyces cerevisiae YNR016c ACC1 acetyl-CoA  
DE carboxylase.  
GN OrderedLocustNames=KLLA0F06072g;  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boisrame A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,



RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.,  
RT "Genome evolution in yeasts";  
RL Nature 430:35-44(2004).  
DR EMBL; CR382126; CAG98063.1; -; Genomic\_DNA.  
DR SMR; Q6CL34; 16-567, 1480-2216.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0009374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF0289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP\_GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS00968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS50989; COA\_CT\_CTER; 1.  
DR PROSITE; PS50980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 2231 AA; 249258 MW; E3C725C1B316941F CRC64;  
  
Query Match 72.3%; Score 2100.5; DB 2; Length 2231;  
Best Local Similarity 70.6%; Pred. No. 4e-134;  
Matches 392; Conservative 72; Mismatches 90; Indels 1; Gaps 1;  
  
QY 6 KAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSKWAYETF 65  
DB 28 KLASHFIGLNTVDKADDSPLKEFKVSHGGHTVTSKVLIANNGIAAVKEIRSVRKWAYETF 87  
  
QY 66 GDERAIEFTVMATPEDLKNVADYIRMDQYVEVPGGSNNNNYANVDLIVDAERAGVHAV 125  
DB 88 GDERTVQFVAMATPEDLEANAEYIRMDQYIEVPGGTNNNNYANVDLIVEAERADVDVAV 147  
  
QY 126 WAGWGHASNPRLPESLAASKHKIIFIGPPGSANRSLGDKISSTIVAQHADVPCMPWSGT 185  
DB 148 WAGWGHASNPRLPERLAASHRKIIFIGPPGNAMRSLGDKISSTIVAQHAQKVCIPWSGT 207  
  
QY 186 GIKETMM-SDQGFLTVSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCT 244  
DB 208 GVDEVHVDKETNLVSVDKVIYQEGCCSPEDGLKAKEIGFPIIMVKASEGGGKGIRKVE 267  
  
QY 245 NGEFEKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQ 304  
DB 268 NEDEFSLYQQAANEIPGSPIFIMKLAGKARHLEVQLLADQYGTNISLFGDCSVQRRHQ 327  
  
QY 305 KIIEEAPVTIAPDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364  
DB 328 KIIEEAPVTIAKPDFTTEMEKAAVRLGQLVGYVSAGTVEYLYSHDEKDFYLELNPRLQV 387  
  
QY 365 EHPPTTEMVSGVNIAPAAQLQVAMGIPLYISIRDIRTLYGMDPRGNEVIDFDFSSPESFKTOR 424

Db 388 EHPTTEMVTGVNLPQAQLQIAMGIPMHRIRDIRLLYGVDPKSASEIDNFESTPESAKTOR 447  
QY 425 KPQPGQHVHVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484  
Db 448 KPTPKGCHCTACRITSEDPNEGFKPGSGGALHELNFRSSSNVWGYFSVGNNGIHSFSDSQF 507  
QY 485 GHIFAYGADRSEARKQMVISLXKELSIKELSGIRGDFRTTVEYLYKLLETFDAFESNKITTTGWLDGLI 544  
Db 508 GHIFAFGENRQASRKHMVVALKELSGIRGDFRTTVEYLYKLLETFEDFEDNTITTTGWLDGLI 567  
  
QY 545 QDRLTAERPPADLAV 559  
Db 568 SQKMTAEKPDRTLSV 582  
  
RESULT 12  
Q6FKK8 CANGA  
AC Q6FKK8 CANGA PRELIMINARY; PRT; 2233 AA.  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Candida glabrata strain CBS138 chromosome L complete sequence.  
GN OrderedLocusNames=CAGL0L10780g;  
OS Candida glabrata (Yeast) (Torulopsis glabrata).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5478;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 2001 / CBS 138;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.;  
RT "Genome evolution in yeasts";  
RL Nature 430:35-44(2004).  
DR EMBL; CR380958; CAG62210.1; -; Genomic\_DNA.  
DR SMR; Q6FKK8; 15-566, 1482-2218.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0009374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP\_GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.



DR	GO; GO:000280; P:nuclear division; IMP.	
DR	InterPro; IPR011761; ATP_GRASP.	
DR	InterPro; IPR011764; BC.	
DR	InterPro; IPR001882; Biotin_BS.	
DR	InterPro; IPR005482; Biotin_carb_C.	
DR	InterPro; IPR000089; Biotin_lipoYL.	
DR	InterPro; IPR000022; Carboxyl_trans.	
DR	InterPro; IPR011763; COA_CT_C.	
DR	InterPro; IPR011762; COA_CT_N.	
DR	InterPro; IPR005481; CPase_L_N.	
DR	InterPro; IPR005479; CPase_D2_ATP_bd.	
DR	Pfam; PF02785; Biotin_carb_C; 1.	
DR	Pfam; PF00364; Biotin_lipoYL; 1.	
DR	Pfam; PF01039; Carboxyl_trans; 1.	
DR	Pfam; PF00289; CPase_L_chain; 1.	
DR	Pfam; PF02786; CPase_L_D2; 1.	
DR	PROSITE; PS50975; ATP_GRASP; 1.	
DR	PROSITE; PS50979; BC; 1.	
DR	PROSITE; PS00188; BIOTIN; 1.	
DR	PROSITE; PS50968; BIOTINYL_LIPOYL; 1.	
DR	PROSITE; PS50989; COA_CT_CTER; 1.	
DR	PROSITE; PS50980; COA_CT_NTER; 1.	
DR	PROSITE; PS00866; CPASE_1; 1.	
DR	PROSITE; PS00867; CPASE_2; 1.	
KW	ATP-binding; Biotin; Complete proteome; Fatty acid biosynthesis;	
KW	Ligase; Lipid synthesis; Multifunctional enzyme; Nucleotide-binding;	
KW	Phosphorylation.	
FT	DOMAIN 68 577 Biotin carboxylation.	
FT	DOMAIN 226 418 ATP-grasp.	
FT	DOMAIN 711 777 Biotinyl/lipoYL.	
FT	DOMAIN 1644 2141 Carboxyltransferase.	
FT	NP_BIND 266 271 ATP (By similarity).	
FT	ACT_SITE 393 393 By similarity.	
FT	BINDING 745 745 Biotin (covalent) (By similarity).	
FT	BINDING 1772 1772 Coenzyme A (By similarity).	
FT	BINDING 2074 2074 Coenzyme A (By similarity).	
FT	BINDING 2076 2076 Coenzyme A (By similarity).	
FT	CONFLICT 14 42 LYAIKATISLPRLFYRLRLTMAPRVASHF -> RFIFIDVL	
FT	CONFLICT 258 258 LISQSISSFSFFILYFINHI (in Ref. 3).	
FT	CONFLICT 339 340 P -> S (in Ref. 1).	
FT	CONFLICT 512 512 IE -> L (in Ref. 1).	
FT	CONFLICT 523 523 A -> S (in Ref. 1).	
FT	CONFLICT 636 639 A -> T (in Ref. 1).	
FT	CONFLICT 998 1005 DNTR -> YRIP (in Ref. 3).	
FT	CONFLICT 1017 1017 LMKSEPST -> SNEVRTIN (in Ref. 3).	
FT	CONFLICT 1073 1073 K -> N (in Ref. 3).	
FT	CONFLICT 1098 1098 R -> H (in Ref. 3).	
FT	CONFLICT 1105 1105 F -> L (in Ref. 3).	
FT	CONFLICT 1362 1362 V -> Y (in Ref. 1).	
FT	CONFLICT 1427 1427 R -> S (in Ref. 1).	
FT	CONFLICT 1444 1444 G -> E (in Ref. 1).	
FT	CONFLICT 1445 1445 F -> C (in Ref. 3).	
FT	CONFLICT 1449 1449 R -> L (in Ref. 3).	
FT	CONFLICT 1451 1451 F -> S (in Ref. 1).	
FT	CONFLICT 1465 1465 I -> F (in Ref. 3).	
FT	CONFLICT 1480 1480 V -> L (in Ref. 3).	
FT	CONFLICT 1485 1485 V -> L (in Ref. 3).	
FT	CONFLICT 1513 1547 PGMHLRPISPTPYPTKEWLQPRRYKAQLMGTFVY -> TW	
FT	CONFLICT 2280 AA; 256843 MW; 8262C9A1A5C8E891 CRC64;	
FT	CONFLICT 71.9%; Score 2090.5; DB 1; Length 2280;	
FT	CONFLICT 71.4%; Pred. No. 2e-133;	
FT	CONFLICT 396; Conservative 62; Mismatches 96; Indels 1; Gaps 1;	
QY	6 KAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAA VKEIRSKWAYETF 65	
Db	37 RVASHFLGNSLDKAPAGVKDYIASHGGHTVITSILIANNGIAA VKEIRSKWAYETF 96	
QY	66 GDERAIEFTVMATPEDLKNADYIRMDAQYVEVPGSGNNNNYANVDLIVDVAERAGVHAV 125	

Db	97 NNERAIKFTVMATPDDLKVNADYIRMDAQYVEVPGSGNNNNYANVELIVDIAERMNVHAV 156	
QY	126 WAGWGCHASENRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQHADVPCMPWSGT 185	
Db	157 WAGWGCHASENPKLPEMLSASSKKIVFIGPPGSAMRSLGDKISSSTIVAQSARVPCMSWGN 216	
QY	186 GIKETWMSDQ-GFLTVDVVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIRKCT 244	
Db	217 ELQVRIDEETNIVTDDVYQACIRSAEAGIAEKGYPVMIKASEGGGKGIRQVT 276	
QY	245 NGEEFKQLYNAVLGEVPGSPVFMKLGAQARHLEVQLLADQYGNALISIFGRDCSVQRRHQ 304	
Db	277 STEKFAQAFQOVLDELPGSPVFMKLGAQARHLEVQILADQYGNLISLFGDRDCSVQRRHQ 336	
QY	305 KIIEEAPVTIAPEDARESMEEKAAVRLAKLVGYVSAGTVWEWLYSPESGEFAFLELNPRLOV 364	
Db	337 KIIEEAPVTIAPATFHEMERAADVRLGELVGYASAGTIEYLYEPENDRFYFLELNPRLOV 396	
QY	365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFESSPESFKTOR 424	
Db	397 EHPTTEMVSGVNLPAALQVAMGLPLSRIPHIRELYGLPRDGDSEIDFFFQNPESFKVQK 456	
QY	425 KPQPGHVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOQ 484	
Db	457 VPTPKGHCVACRITSEDPGEGFKPSSGMKDLNFRSSNNWGYFVGTAGIHEFADSOQ 516	
QY	485 GHIFAYGADRSEARKQMVISLKELSGIRGDFRTTVEYLIKLETFDAFESNKITTGWLDGLI 544	
Db	517 GHIFSFAESRESSKSMVVALKELSGIRGDFRTTVEYLVRLLETKEPSENEFTTGWLDRLI 576	
QY	545 QDRLTAERPPADLAV 559	
Db	577 AQKVTARPPDKMLAV 591	
RESULT 14		
Q6CC91_YARLI	PRELIMINARY; PRT; 2266 AA.	
ID	Q6CC91_YARLI	
AC	Q6CC91;	
DT	25-OCT-2004 (TrEMBLrel. 28, Created)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Similar to sp Q00955 Saccharomyces cerevisiae Acetyl-CoA	
DE	carboxylase.	
GN	OrderedLocusNames=YALI0C11407g;	
OS	Yarrowia lipolytica (Candida lipolytica).	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
OC	Saccharomycetales; Dipodascaceae; Yarrowia.	
OX	NCBI_TaxID=4952;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=CLIB 122 / E 150;	
RX	PubMed=15229592; DOI=10.1038/nature02579;	
RA	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,	
RA	Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,	
RA	Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,	
RA	Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,	
RA	Boisrame A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,	
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,	
RA	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,	
RA	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,	
RA	Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,	
RA	Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	
RA	Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,	
RA	Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	
RA	Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,	
RA	Wincker P., Souciet J.-L.;	
RT	"Genome evolution in yeasts."	
RL	Nature 430:35-44(2004).	
DR	EMBL; CR382129; CAG82031.1; -; Genomic_DNA.	
DR	SMR; Q6CC91; 33-574.	
DR	GO; GO:0005524; F:ATP binding; IEA.	
DR	GO; GO:0009374; F:biotin binding; IEA.	



DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP\_GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; UNKNOWN\_1.  
DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS50989; COA\_CT\_CTER; 1.  
DR PROSITE; PS50980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 2266 AA; 251115 MW; 8B581AF5F9374E4A CRC64;

Query Match 71.7%; Score 2084; DB 2; Length 2266;  
Best Local Similarity 71.2%; Pred. No. 5.4e-133;  
Matches 399; Conservative 63; Mismatches 96; Indels 2; Gaps 2;  
QY 2 PPDHKA-V-SQFIGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKW 60  
Db 30 PNIHKLGLASHFFGLNSVHTAKPSKVFVASHGGHTVINKVLIANNGLAAVKEIRSIRKW 89  
QY 61 AYETFGDERAIEFTVMATPEDLKNVADYIRNADQYVEVPGGSSNNNNYANVDLIVDAERA 120  
Db 90 AYETFGDERAISFTVMATPEDLAANADYIRNADQYVEVPGGTTNNNNYANVELIVDAERF 149  
QY 121 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180  
Db 150 GVDVAVWAGWGHASENPLLPESLAASPRKIVFIPGPGAAMRSLGDKISSTIVAQAHKVPCI 209  
QY 181 PWSGTGIKETMM-SDQGFLTVSDDDVYQQACIHTAEEGLEKAKEKIGYPMIKASEGGGKG 239  
Db 210 PWSGTGDEVVVDKSTNLVSVSEEVYTKGCTTGPQGLEKAKQIGFPMIKASEGGGKG 269  
QY 240 IRKCTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSV 299  
Db 270 IRKVEREEDFEAAHYHQVEGEIPGSPFIFIMQLAGNARHLEVQLLADQYGNALISIFGRDCSV 329  
QY 300 QRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELN 359  
Db 330 QRRHQKIIIEEAPVTIVAGQOFTTAMEKAAVRLGKLVGYVSAGTVEYLYSHEDDKFYFLELN 389  
QY 360 PRLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPES 419  
Db 390 PRLOVEHPTTEMVTGNLPAAQLQIAMGIPLDRIKDIRLFYGVNPHHTTPIIDFSGEDA 449  
QY 420 FKTQKPPQPOGHVACRITAENPDGFKPGMGALTELNFRSSTSTWYFVSFGTSGALHEY 479  
Db 450 DKTQRRPVPRGHTTACRITSEDPGEGFKPSGGTMHNLNFRSSSNVWYFVSNGQGIHSF 509  
QY 480 ADSQFGHIFAYGADRSEARKQMVISLKELSGDFRTTVEYLIKLETDAPESNKIITGW 539  
Db 510 SDSQFGHIFAFGENRSASRKHMMVALKELSGDFRTTVEYLIKLETPDFEDNTIITGW 569  
QY 540 LDGLIQDRLTAERPDLAV 559  
Db 570 LDELISNKLTAERPDSFLAV 589

RESULT 15  
Q75EK8 ASHGO  
ID Q75EK8 ASHGO PRELIMINARY; PRT; 2231 AA.  
AC Q75EK8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE AAR071WP.  
GN Name=AAR071W;  
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.  
OX NCBI\_TaxID=33169;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 10895;  
RX PubMed=15001715; DOI=10.1126/science.1095781;  
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,  
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavie A.,  
RA Gaffney T.D., Philippsen P.;  
RT "The Ashbya gossypii genome as a tool for mapping the ancient  
RT Saccharomyces cerevisiae genome.";  
RL Science 304:304-307(2004).  
DR EMBL; AE016814; AAS50436.1; -; Genomic\_DNA.  
DR SMR; Q75EK8; 16-566, 1480-2216.  
DR AGD; AAR071W; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:000374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP\_GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS50989; COA\_CT\_CTER; 1.  
DR PROSITE; PS50980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 2231 AA; 249717 MW; 5024EA7C7873B842 CRC64;

Query Match 71.2%; Score 2069.5; DB 2; Length 2231;  
Best Local Similarity 70.4%; Pred. No. 5.2e-132;  
Matches 387; Conservative 71; Mismatches 91; Indels 1; Gaps 1;  
QY 11 FTGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWYETFGDERA 70  
Db 32 FGLNTVEQAEASPLRDYVRLHGGHTVISKILIANNGIAAVKEIRSIRKWYETFGDGKV 91  
QY 71 IEPTVMATPEDLKNVADYIRNADQYVEVPGGSSNNNNYANVDLIVDAERAGVHAVWAGW 130  
Db 92 VQFVVMATPEDLEANTEYIRNADQYVEVPGGTTNNNNYANVDLIVDAERADVDVAVWAGW 151  
QY 131 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGIKET 190  
Db 152 HASENPLLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCIPWSGTGVDQV 211  
QY 191 MMSDQ-GFLTVDVYQQACIHTAEEGLEKAKEKIGYPMIKASEGGGKGIRKCTNGEEF 249



OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 2015-2022.  
RX MEDLINE=92262474; PubMed=1350093;  
RA Al-Feel W., Chirala S.S., Wakil S.J.;  
RT "Cloning of the yeast FAS3 gene and primary structure of yeast acetyl-  
RT CoA carboxylase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:4534-4538(1992).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=97313269; PubMed=9169873;  
RA Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K.,  
RA Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K.,  
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,  
RA Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,  
RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F.,  
RA Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,  
RA Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,  
RA Goffeau A., Gueldener U., Herbert C.J., Heumann K., Heuss-Neitzel D.,  
RA Hilbert H., Himni K., Iraqui Houssaini I., Jacquet M., Jimenez A.,  
RA Jonniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,  
RA Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,  
RA Messenguy F., Mewes H.-W., Moestl D., Naer F., Nicaud J.-M.,  
RA Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J.,  
RA Pohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L.,  
RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,  
RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhasselt P.,  
RA Vierendeels F., Visser S., Voet M., Volckaert G., Wach A.,  
RA Wambutt R., Wedler H., Zollner A., Hani J.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV  
RT and its evolutionary implications.";  
RL Nature 387:93-98(1997).  
RN [3]  
RP PHOSPHORYLATION SITE SER-1157.  
RX MEDLINE=21864552; PubMed=11875433; DOI=10.1038/nbt0302-301;  
RA Picarro S.B., McClelland M.L.; Stukenberg P.T., Burke D.J., Ross M.M.,  
RA Shabanowitz J., Hunt D.F., White F.M.;  
RT "Phosphoproteome analysis by mass spectrometry and its application to  
RT Saccharomyces cerevisiae.";  
RL Nat. Biotechnol. 20:301-305(2002).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1429-2233 IN COMPLEX WITH  
RP COA, MUTAGENESIS OF LEU-1705; ARG-1731; TYR-1738 AND ARG-1954, AND  
RP HOMODIMERIZATION.  
RX PubMed=12663926; DOI=10.1126/science.1081366;  
RA Zhang H., Yang Z., Shen Y., Tong L.;  
RT "Crystal structure of the carboxyltransferase domain of acetyl-  
RT coenzyme A carboxylase.";  
RL Science 299:2064-2067(2003).  
CC -!- FUNCTION: This protein carries three functions: biotin carboxyl  
CC carrier protein, biotin carboxylase, and carboxyltransferase.  
CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate  
CC + malonyl-CoA.  
CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)  
CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.  
CC -!- COFACTOR: Biotin.  
CC -!- ENZYME REGULATION: By phosphorylation.  
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)  
CC step.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Contains 1 ATP-grasp domain.  
CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.  
CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.  
CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC EMBL; M92156; AAA20073.1; -; Unassigned DNA.  
DR EMBL; Z71631; CAA96294.1; -; Genomic DNA.  
DR PIR; S63347; S63347.  
DR PDB; 1OD2; X-ray; A/B=1429-2233.  
DR PDB; 1OD4; X-ray; A/B/C=1429-2233.  
DR PDB; 1UYR; X-ray; A/B=1482-2218.  
DR PDB; 1UYS; X-ray; A/B/C=1482-2218.  
DR PDB; 1UYT; X-ray; A/B=-.  
DR PDB; 1UYV; X-ray; A/B=-.  
DR PDB; 1W2X; X-ray; A/B/C=1476-2233.  
DR PDB; 1W93; X-ray; A=14-566.  
DR PDB; 1W96; X-ray; A/B/C=13-566.  
DR SMR; Q00955; 14-566.  
DR IntAct; Q00955; -.  
DR GerMOnline; 143361; -.  
DR Ensembl; YNR016C; Saccharomyces cerevisiae.  
DR SGD; S000005299; ACC1.  
DR GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.  
DR GO; GO:0005739; C:mitochondrion; IDA.  
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IMP.  
DR GO; GO:0004075; F:biotin carboxylase activity; IMP.  
DR GO; GO:0006998; P:nuclear membrane organization and biogenesis; TAS.  
DR GO; GO:0006506; P:protein-nucleus import; IMP.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_Carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPSase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS00975; ATP\_GRASP; 1.  
DR PROSITE; PS00979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS00968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS00989; COA\_CT\_CTER; 1.  
DR PROSITE; PS00980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; 1.  
DR PROSITE; PS00867; CPSASE\_2; 1.  
KW 3D-structure; ATP-binding; Biotin; Complete proteome;  
KW Direct protein sequencing; Fatty acid biosynthesis; Ligase;  
KW Lipid synthesis; Multifunctional enzyme; Nucleotide-binding;  
KW Phosphorylation.  
FT DOMAIN 58 567 Biotin carboxylation.  
FT DOMAIN 216 408 ATP-grasp.  
FT DOMAIN 701 767 Biotinyl/lipoyl.  
FT DOMAIN 1603 2101 Carboxyltransferase.  
FT NP\_BIND 256 261 ATP (By similarity).  
FT ACT\_SITE 383 383 By similarity.  
FT BINDING 735 735 Biotin (covalent) (By similarity).  
FT BINDING 1731 1731 Coenzyme A.  
FT BINDING 2034 2034 Coenzyme A.  
FT BINDING 2036 2036 Coenzyme A.  
FT MOD\_RES 1157 1157 Phosphoserine.  
FT MUTAGEN 1705 1705 L->I: Raises Km for malonyl-CoA by a  
FT factor of 20.  
FT MUTAGEN 1731 1731 R->S: Raises Km for malonyl-CoA by a  
FT factor of 15.  
FT MUTAGEN 1738 1738 Y->F: No effect.  
FT MUTAGEN 1954 1954 R->S: Raises Km for malonyl-CoA by a  
FT factor of 70.  
FT MUTAGEN 1994 1994 E->Q: Lowers activity 10-fold.  
FT CONFLICT 1523 1523 W -> G (in Ref. 1).  
FT CONFLICT 1755 1755 I -> IWYRCL (in Ref. 1).  
FT CONFLICT 1761 1766 AINKML -> ESTNA (in Ref. 1).



SQ SEQUENCE 2233 AA; 250353 MW; 0A335AAD9B1F8308 CRC64;  
Query Match 70.9%; Score 2060; DB 1; Length 2233;  
Best Local Similarity 69.1%; Pred. No. 2.3e-131;  
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;  
QY 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAATKESIRKWAY 62  
DB 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAATKESIRKWAY 83  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGV 122  
DB 84 ETFGDDRTVQFVAMATPEDLEANAIEYIRMDQYIEVPGGNNNNYANVDLIVDAERADV 143  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPCMPW 182  
DB 144 DAVWAGWGHASENPLLPESLQSKRKVIFIGPPGNAMRSLGDKISSITVAQSAKVPCIPW 203  
QY 183 SGTGIKETMMSDQ--GFLTVDVDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240  
DB 204 SGTGV-DTVHVDKTLGLSVDDDIYQKGCCTSPDGLQAKRIGFPVMIKASEGGGKGI 262  
QY 241 RKCTNGEEFKQLYNVAVLGEVPGSPVFMVKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
DB 263 ROVEREEDFIALYHOANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNLSLFGDRDCSVQ 322  
QY 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
DB 323 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLKLVGYVSAGTVEWLYSHDDGKFYFLELNP 382  
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVIDFDFSSPESF 420  
DB 383 RLQVEHPTTEMVSGVNLPAALQIAAGIPMHRISDITRTLYGMNPHSASEIDFEFTQDAT 442  
QY 421 KTORKPQPGHVHVACRITAENPDGTGKPGMGALTELNFERSSTSTGWYFVCTSGALHEYA 480  
DB 443 KQORRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRRSSNVWGVSVGNNGNIHSFS 502  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAPESNKITTGWL 540  
DB 503 DSQFGHIFAFGENRQASRKGMVVALKELSIKRGDFRTTVEYLIKLLETFEDNTITTGWL 562  
QY 541 DGLIQDRLTAERPPADLAV 559  
DB 563 DDLITHKMTAEKPDPTLAV 581

RESULT 18  
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AC Q6BX58;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to CA5816|CaAC1 Candida albicans CaAC1 acetyl-coenzyme-A  
DE carboxylase.  
GN OrderedLocusNames=DEHA0B056329;  
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.  
OX NCBI\_TaxID=4959;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 36239 / CBS 767;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boisrame A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.;  
RT "Genome evolution in yeasts.";  
RL Nature 430:35-44 (2004).  
DR EMBL; CR382134; CAG85206.1; -; Genomic\_DNA.  
DR SMR; Q6BX58; 79-628, 1547-2257.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0009374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
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DR InterPro; IPR005482; Biotin\_carb\_C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CPase\_D2\_ATP\_bd.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPase\_L\_chain; 1.  
DR Pfam; PF02786; CPase\_L\_D2; 1.  
DR PROSITE; PS0975; ATP\_GRASP; 1.  
DR PROSITE; PS0979; BC; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS0968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS0989; COA\_CT\_CTER; 1.  
DR PROSITE; PS0980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPASE\_2; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 2297 AA; 257947 MW; 0E766966E5C4CB33 CRC64;

Query Match 70.2%; Score 2039.5; DB 2; Length 2297;  
Best Local Similarity 69.4%; Pred. No. 6.1e-130;  
Matches 385; Conservative 72; Mismatches 97; Indels 1; Gaps 1;  
QY 6 KAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAATKESIRKWAYETF 65  
DB 89 KLADHFKGLNSADNAEPKVTDFVRSHEGHTVISRVLIANNGLAAVKEIRSVRKWAYETF 148  
QY 66 GDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHAV 125  
DB 149 GDERAIEFTVMATPEDLEANAIEYIRMDQYIEVPGGNNNNYANVDLIVDAERTNVDVAV 208  
QY 126 WAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPCMPWSGT 185  
DB 209 WAGWGHASENPLLPESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPCIPWSGT 268  
QY 186 GIKETMMSDQ-GFLTVDVDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCT 244  
DB 269 GVREVKIDEETNLVSVSDAVYAKGCCTSPDGLVKAKEIGFPVMIKASEGGGKGIKVD 328  
QY 245 NGEFFKQLYNVAVLGEVPGSPVFMVKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQ 304  
DB 329 NEKDFIALYKQASNEIPGSPIFIMKLAGDARHLEVQLLADQYGTNLSLFGDRDCSVORRHQ 388  
QY 305 KIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364  
DB 389 KIEEAPVTIAKKESFHAMENAAVRLKLVGYVSAGTVEWLYSHSEDKFYFLELNPRLQV 448  
QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVIDFDFSSPESFQTR 424  
DB 449 EHPTTEMVGTGNLPAALQIAAGIPMHRIRDIRSLYGVDPHTSTEIDFEFKTESLSVSR 508  
QY 425 KPQPQGHVVACRITAENPDGTGFKPGMGALTELNFRRSSSTSTGWYFVCTSGALHEYADSQF 484

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Db 509 RVPKGGTTACRITSEDPGEFGKPSGSLHFNFRSSNVWGYFSVGNQSSIHSFSDSQF 568
Qy 485 GHIPAYGADRSEARKQMVISLKELSGRDFRTTVEYLKLETDAFESNKITTTGWLGLI 544
Db 569 GHIPAFGENRSASRKMVMVALKELSGRDFRTTVEYLKLETDPTDFEDNTITTTGWLDELI 628
Qy 545 QDRLTAEPPADLAV 559
Db 629 SKXLTSEPDHIVAV 643

RESULT 19
HFAL YEAST
ID HFAL YEAST STANDARD; PRT; 2273 AA.
AC P32874;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE HFAL protein.
GN Name=HFAL; OrderedLocusNames=YMR207C; ORFNames=YMR8261.01C, YMR8325.08C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 125-949.
RX MEDLINE=94146412; PubMed=7906156;
RA Kearsey S.E.;
RT "Identification of a Saccharomyces cerevisiae gene closely related to
RT FAS3 (acetyl-CoA carboxylase).";
RL DNA Seq. 4:69-70 (1993).
CC -!- COFACTOR: Biotin (By similarity).
CC -!- SIMILARITY: Contains 1 ATP-grasp domain.
CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.
CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.
CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.
CC -!- CAUTION: The reading frame from which this protein in translated
CC has no Met initiation codon near to the 5' end. It does not seem to
CC be a pseudogene. There are no apparent frameshifts.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z49809; CAA89922.1; -; Genomic DNA.
CC EMBL; Z48755; CAA88647.1; -; Genomic DNA.
CC EMBL; Z22558; CAA80280.1; -; Genomic DNA.
CC PIR; S55089; S55089.
CC HSSP; Q00955; 1OD4.
CC SMR; P32874; 90-634.
CC GerMOnline; 142882; -.
CC Ensemble; YMR207C; Saccharomyces cerevisiae.
CC SGD; S000004820; HFAL.
CC GO; GO:0005739; C:mitochondrion; IDA.
CC GO; GO:0003989; F:acetyl-CoA carboxylase activity; IGI.
CC GO; GO:0006633; P:fatty acid biosynthesis; IGI.
CC InterPro; IPR011761; ATP_GRASP.
CC InterPro; IPR011764; BC.
CC InterPro; IPR001882; Biotin_BS.
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DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR011763; COA_CT_C.
DR InterPro; IPR011762; COA_CT_N.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR005479; CPase_D2_ATP_bd.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR PROSITE; PS50975; ATP_GRASP; 1.
DR PROSITE; PS50979; BC; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS50968; BIOTINYL_LIPOYL; 1.
DR PROSITE; PS50989; COA_CT_CTER; 1.
DR PROSITE; PS50980; COA_CT_NTER; 1.
DR PROSITE; PS00866; CPASE_1; 1.
DR PROSITE; PS00867; CPASE_2; 1.
KW ATP-binding; Biotin; Complete proteome; Ligase; Nucleotide-binding.
FT DOMAIN 134 635 Biotin carboxylation.
FT DOMAIN 292 484 ATP-grasp.
FT DOMAIN 770 836 Biotinyl/lipoyl.
FT DOMAIN 1648 2147 Carboxyltransferase.
FT NP_BIND 332 337 ATP (By similarity).
FT ACT_SITE 459 459 By similarity.
FT BINDING 804 804 Biotin (covalent) (By similarity).
FT CONFLICT 661 661 F -> L (in Ref. 2).
SQ SEQUENCE 2273 AA; 259163 MW; 08727A301549DA92 CRC64;

Query Match 65.0%; Score 1889.5; DB 1; Length 2273;
Best Local Similarity 64.3%; Pred. NO. 1.1e-119;
Matches 355; Conservative 86; Mismatches 94; Indels 17; Gaps .4;

Qy 2 PPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWA 61
Db 105 PP-----QFIGLNTVESAQPSILRDFVLRGGHTVISKILIANNGIAAVKEIRSRKWA 158
Qy 62 YETFGDERAIEFTVMATPEDLKVNADYIRMDADQYVEVPGSGNNNNYANVDLIVDVAERAG 121
Db 159 YETFNDEKIIQFVVMATPDDLHANSEYIRMDADQYVQVPGGTNNNNYANIDLIDVAEQTD 218
Qy 122 VHAWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPCMP 181
Db 219 VDAVWAGWGHASENCPPELLASSQRKILFIGPPGRAMRSLGDKISSITVAQSAKIPICP 278
Qy 182 WSGTGIGKETMMSDQ--GFLTVDSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKG 239
Db 279 WSGSHI-DTIHIDNKTNFVSPDDVYVRGCCSPEDALEKAKLIGFPVMIKASEGGGKG 337
Qy 240 IRKCTNGEEFKQLYNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSV 299
Db 338 IRRVDNEDDFIALYRQAVNETPGSPFMVVKVVTDAHLEVQLLADQYGTNITLFGRDCSI 397
Qy 300 QRRHQKIIIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELN 359
Db 398 QRRHQKIIIEEAPVTITKPETFORMERAIRLGELVGYVSAGTVEYLYSPKDDKFYFLELN 457
Qy 360 PRLOVEHPTTEMVSGVNI PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPES 419
Db 458 PRLOVEHPTTEMISGVNLPATQLQIAMGIPMHMISDIRKLYGLDPTGTSYID----- 509
Qy 420 FKTQKPKPQGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEY 479
Db 510 FKNLKRSPKPGHCISCRTISEDPNEGFKPSTGKIHELNFRSSSNVWGYFSVGNNGAIHSF 569
Qy 480 ADSQFGHIFAYGADRSEARKQMVISLKELSGRDFRTTVEYLKLETDAFESNKITTTGW 539
Db 570 SDSQFGHIFAVGNDRQDAKQNMVLAALKDPSIRGEFKTPIEYLIELLETRDFESNNISTGW 629
Qy 540 LDGLIQDRLTAE 551
||| ||| |||
```

Db	630	LDDLILKNLSSD	641	
RESULT 20				
O42823	YEAST			
ID	O42823_YEAST	PRELIMINARY;	PRT;	2273 AA.
AC	O42823;			
DT	01-JUN-1998	(TrEMBLrel. 06, Created)		
DT	01-JUN-1998	(TrEMBLrel. 06, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Acetyl-coenzyme A carboxylase like carboxylase (Fragment).			
GN	Name=ALC;			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=SP1;			
RA	Saito A., Kazuta Y., Kondo H., Tanabe T.;			
RL	Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL;	D78165; BAA24410.1; -; Genomic_DNA.		
DR	HSSP;	Q00955; 10D4.		
DR	SMR;	O42823; 90-634.		
DR	Ensembl;	YMR207C; Saccharomyces cerevisiae.		
DR	GO;	GO:0005524; F:ATP binding; IEA.		
DR	GO;	GO:0009374; F:biotin binding; IEA.		
DR	GO;	GO:0016874; F:ligase activity; IEA.		
DR	GO;	GO:0008152; P:metabolism; IEA.		
DR	InterPro;	IPR011761; ATP_GRASP.		
DR	InterPro;	IPR011764; BC.		
DR	InterPro;	IPR001882; Biotin_BS.		
DR	InterPro;	IPR005482; Biotin_carb_C.		
DR	InterPro;	IPR000089; Biotin_lipoyl.		
DR	InterPro;	IPR000022; Carboxyl_trans.		
DR	InterPro;	IPR011763; COA_CT_C.		
DR	InterPro;	IPR011762; COA_CT_N.		
DR	InterPro;	IPR005481; CPase_L_N.		
DR	InterPro;	IPR005479; Cphp_synth_L_D2.		
DR	Pfam;	PF02785; Biotin_carb_C; 1.		
DR	Pfam;	PF00364; Biotin_lipoyl; 1.		
DR	Pfam;	PF01039; Carboxyl_trans; 1.		
DR	Pfam;	PF00289; CPase_L_chain; 1.		
DR	Pfam;	PF02786; CPase_L_D2; 1.		
DR	PROSITE;	PS50975; ATP_GRASP; 1.		
DR	PROSITE;	PS50979; BC; 1.		
DR	PROSITE;	PS00188; BIOTIN; 1.		
DR	PROSITE;	PS0968; BIOTINYL_LIPOYL; 1.		
DR	PROSITE;	PS0989; COA_CT_CTER; 1.		
DR	PROSITE;	PS0980; COA_CT_NTER; 1.		
DR	PROSITE;	PS00866; CPASE_1; UNKNOWN_1.		
DR	PROSITE;	PS00867; CPASE_2; UNKNOWN_1.		
KW	Biotin.			
FT	NON_TER	1		
SQ	SEQUENCE	2273 AA; 259162 MW; BF6C01982FCB5DEF	CRC64;	
Query Match				
Best local Similarity 65.0%; Score 1889.5; DB 2; Length 2273;				
Matches 355; Conservativity 64.3%; Pred. No. 1.le-119;				
Matches 355; Conservative 86; Mismatches 94; Indels 17; Gaps 4;				
QY	2	PPDHKAVSQFIGGNPLETAPASPVADFIRKQGHSVITKVLICNNGIAAVKEIRSIRKWA	61	
Db	105	PP-----QFIGLNTVESAQPSILRDFVLRGGHTVISKILIANNGIAAVKEMRSIRKWA	158	
QY	62	YETFGDERAIEFTVMATPEDLKNVADYIRMADQYVEVPGSGNNNNYANVDLIYDVAERAG	121	
Db	159	YETFNDEKIIQFVVMATPDDLHANSEYIRMADQYVQVPGGTNNNNYANIDLIDVAEQTD	218	
QY	122	VHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMP	181	
Db	219	VDAVWAGWGHASENPLPELLASSQRKILFIGPGRAMRSLGDKISSTIVAQSAKIPCIP	278	
QY	182	WSGTGKETWMSDQ--GFLTVDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKG	239	
Db	279	WSGSHI-DTIHIDNKNFVSPDDVYVRGCCSSPEDALEKAKLIGFPVMIKASEGGGKG	337	
QY	240	IRKCTNGEEFKQLYNVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSV	299	
Db	338	IRRVNEDDDFIALYRQAVNETPGSPFMVKVVTDAHLEVQLLADQYGTNITLFGDRDCSI	397	
QY	300	QRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGVYSAGTVEWLYSPESGEFAFLELN	359	
Db	398	QRRHQKIIIEEAPVTITKPTFORMERAAIRLGELVGVYSAGTVEYLYSPKDDKIFYFLELN	457	
QY	360	PRLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSTDIRTLYGMDPRGNEVIDDFESSPES	419	
Db	458	PRLOVEHPTTEMISGVNLPATQLQIAMGIPMEMISDIRKLYGLDPTGTSYID-----	509	
QY	420	FKTQKQPQGHVHVACRITAENPDTGFKPGMGALTFLNFRSSTSTWGYFVSGTSGALHEY	479	
Db	510	FKNLKRPSPKGHCISCRTSEDNPEGFKPSTGKIHELNFRSSNVWGYFVSGNNGAIHSF	569	
QY	480	ADSQFGHIFAYGADRSEARKQMVISLKELSGIRGDFRTTVEYLIKLETDAFESNKITGW	539	
Db	570	SDSQFGHIFAVGNDRQDAKQNMVLALKDPSIRGEFKTPIEYLIELLETRDFESNNISTGW	629	
QY	540	LDGLIQDRLTAE	551	
Db	630	LDDLILKNLSSD	641	
RESULT 21				
Q6XDA8	HUMAN			
ID	Q6XDA8_HUMAN	PRELIMINARY;	PRT;	2346 AA.
AC	Q6XDA8;			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Acetyl-CoA carboxylase.alpha.			
GN	Name=ACACA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Sinilnikova O.M., Ginolhac S.M., Magnard C., Leone M., Anczukow O.,			
RA	Moreau K., Thompson D., Coutanson C., Bonadona V., Lasset C.,			
RA	Goldgar D.E., Joulin V., Dalla Venezia N., Lenoir G.M.;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL;	AY237919; AAP69841.1; -; mRNA.		
DR	Ensembl;	ENSG00000132142; Homo sapiens.		
DR	GO;	GO:0005524; F:ATP binding; IEA.		
DR	GO;	GO:0009374; F:biotin binding; IEA.		
DR	GO;	GO:0016874; F:ligase activity; IEA.		
DR	GO;	GO:0008152; P:metabolism; IEA.		
DR	InterPro;	IPR011761; ATP_GRASP.		
DR	InterPro;	IPR011764; BC.		
DR	InterPro;	IPR001882; Biotin_BS.		
DR	InterPro;	IPR005482; Biotin_carb_C.		
DR	InterPro;	IPR000089; Biotin_lipoyl.		
DR	InterPro;	IPR000022; Carboxyl_trans.		
DR	InterPro;	IPR011763; COA_CT_C.		
DR	InterPro;	IPR011762; COA_CT_N.		
DR	InterPro;	IPR005481; CPase_L_N.		
DR	InterPro;	IPR005479; CPase_D2_ATP_bd.		
DR	Pfam;	PF02785; Biotin_carb_C; 1.		
DR	Pfam;	PF00364; Biotin_lipoyl; 1.		
DR	Pfam;	PF01039; Carboxyl_trans; 1.		
DR	Pfam;	PF00289; CPase_L_chain; 1.		
DR	Pfam;	PF02786; CPase_L_D2; 1.		
DR	PROSITE;	PS50975; ATP_GRASP; 1.		
DR	PROSITE;	PS50979; BC; 1.		
DR	PROSITE;	PS00188; BIOTIN; 1.		
DR	PROSITE;	PS50968; BIOTINYL_LIPOYL; 1.		





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Db          632 V 632
RESULT 23
COAL_RAT
ID COAL_RAT STANDARD; PRT; 2345 AA.
AC P11497; P97902;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin
DE carboxylase (EC 6.3.4.14)].
GN Name=Acaca; Synonyms=ACAC;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=88320328; PubMed=2901088;
RA Lopez-Casillas F., Bai D.-H., Luo X., Kong I.-S., Hermodson M.A.,
RA Kim K.-H.;
RT "Structure of the coding sequence and primary amino acid sequence of
RT acetyl-coenzyme A carboxylase."
RL Proc. Natl. Acad. Sci. U.S.A. 85:5784-5788(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=89264558; PubMed=2566999;
RA Luo X.N., Park K., Lopez-Casillas F., Kim K.-H.;
RT "Structural features of the acetyl-CoA carboxylase gene: mechanisms
RT for the generation of mRNAs with 5' end heterogeneity."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4042-4046(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-33.
RX MEDLINE=89214151; PubMed=2565337;
RA Lopez-Casillas F., Kim K.-H.;
RT "Heterogeneity at the 5' end of rat acetyl-coenzyme A carboxylase
RT mRNA. Lipogenic conditions enhance synthesis of a unique mRNA in
RT liver."
RL J. Biol. Chem. 264:7176-7184(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1167-1200 (ISOFORMS 1 AND 2), AND
RP PHOSPHORYLATION SITE SER-1200.
RX MEDLINE=90337981; PubMed=1974251;
RA Kong I.-S., Lopez-Casillas F., Kim K.-H.;
RT "Acetyl-CoA carboxylase mRNA species with or without inhibitory coding
RT sequence for Ser-1200 phosphorylation."
RL J. Biol. Chem. 265:13695-13701(1990).
RN [5]
RP BIOTIN-BINDING SITE.
RX MEDLINE=89289706; PubMed=2567668;
RA Bai D.-H., Moon T.-W., Lopez-Casillas F., Andrews P.C., Kim K.-H.;
RT "Analysis of the biotin-binding site on acetyl-CoA carboxylase from
RT rat."
RL Eur. J. Biochem. 182:239-245(1989).
RN [6]
RP PROTEIN SEQUENCE OF 76-85 AND 1198-1201, AND PHOSPHORYLATION.
RX MEDLINE=88296498; PubMed=2900138;
RA Munday M.R., Campbell D.G., Carling D., Hardie D.G.;
RT "Identification by amino acid sequencing of three major regulatory
RT phosphorylation sites on rat acetyl-CoA carboxylase."
RL Eur. J. Biochem. 175:331-338(1988).
RN [7]
RP PARTIAL PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=94237850; PubMed=7910165;
RA Winz R., Hess D., Aebersold R., Brownsey R.W.;
RT "Unique structural features and differential phosphorylation of the
RT 280-kDa component (isozyme) of rat liver acetyl-CoA carboxylase."
RL J. Biol. Chem. 269:14438-14445(1994).
CC -!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis
of long-chain fatty acids. This protein carries three functions:
biotin carboxyl carrier protein, biotin carboxylase, and
carboxyltransferase.
-!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
+ malonyl-CoA.
-!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
= ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
-!- COFACTOR: Biotin.
-!- ENZYME REGULATION: By phosphorylation.
-!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
step.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=P11497-1; Sequence=Displayed;
Name=2;
IsoId=P11497-2; Sequence=VSP_011753;
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Contains 1 ATP-grasp domain.
-!- SIMILARITY: Contains 1 biotin carboxylation domain.
-!- SIMILARITY: Contains 1 biotinyl-binding domain.
-!- SIMILARITY: Contains 1 carboxyltransferase domain.
-----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; J03808; AAA40653.1; -; mRNA.
EMBL; M26731; AAA40652.1; -; Genomic_DNA.
EMBL; M26195; AAA40654.1; -; mRNA.
EMBL; M26196; AAA40655.1; -; mRNA.
EMBL; M26197; AAA40656.1; -; mRNA.
EMBL; M55315; -; NOT_ANNOTATED_CDS; mRNA.
PIR; A35578; A35578.
HSSP; Q00955; 1OD4.
Ensembl; ENSRNOG00000034013; Rattus norvegicus.
RGD; 621248; Acac.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin_BS.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000022; Carboxyl_trans.
InterPro; IPR011763; COA_CT_N.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPase_L_N.
InterPro; IPR005479; CPase_D2_ATP_bd.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; Biotin_lipoyl; 1.
Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF00289; CPase_L_chain; 1.
Pfam; PF02786; CPase_L_D2; 1.
PROSITE; PS0975; ATP_GRASP; 1.
PROSITE; PS0979; BC; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS0968; BIOTINYL_LIPOYL; 1.
PROSITE; PS0989; COA_CT_CTER; 1.
PROSITE; PS0980; COA_CT_NTER; 1.
PROSITE; PS00866; CPASE_1; 1.
PROSITE; PS00867; CPASE_2; 1.
KW Alternative splicing; ATP-binding; Biotin; Direct protein sequencing;
KW Fatty acid biosynthesis; Ligase; Lipid synthesis;
KW Multifunctional enzyme; Nucleotide-binding; Phosphorylation.
FT DOMAIN 116 617 Biotin carboxylation.
FT DOMAIN 274 465 ATP-grasp.
FT DOMAIN 751 817 Biotinyl/lipoyl.
FT DOMAIN 1697 2193 Carboxyltransferase.
FT NP_BIND 314 319 ATP (Potential).
FT ACT_SITE 440 440 By similarity.
FT BINDING 785 785 Biotin (covalent).
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FT BINDING 1822 1822 Coenzyme A (By similarity).  
FT BINDING 2126 2126 Coenzyme A (By similarity).  
FT BINDING 2128 2128 Coenzyme A (By similarity).  
FT MOD\_RES 77 77 Phosphoserine.  
FT MOD\_RES 79 79 Phosphoserine.  
FT MOD\_RES 1200 1200 Phosphoserine.  
FT VARSPLOC 1189 1196 Missing (in isoform 2).  
FT FTID=VSP 011753.  
SQ SEQUENCE 2345 AA; 265194 MW; 78E9CF9ADE1E8771 CRC64;

Query Match 61.4%; Score 1785; DB 1; Length 2345;  
Best Local Similarity 63.6%; Pred. No. 1.5e-112;  
Matches 344; Conservative 80; Mismatches 103; Indels 14; Gaps 5;

Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
Db 102 ASP-AEFVTRFGGNKVKIEKVLIANNGIAAVKCMRSIRRSYEMFRNERAIRFVVMVTPED 160  
Qy 82 LKVNADYIRMAQYVEVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLPES 141  
Db 161 LKANAIEYIKMADHYVPVPGGANNNNYANVELILDIKRIPIVQAVWAGWGHASENPKLP 220  
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---QGFL 198  
Db 221 LL--KNGIAFMGPPSQAMWALGDKIASIVAQTAGIPTLPWSGSLRVDWQENDEFSKRIL 278  
Qy 199 TVSDDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALG 258  
Db 279 NVPOQLYERGVYKVDVDDGLKAAEEVGYPMIKASEGGGKGIRKVNADDFPNLFRQVQA 338  
Qy 259 EVPGSPVFMKLAGQARHLEVQILLADQYGNNAISIFGRDCSVORRHQKIEEAPVTIAPED 318  
Db 339 EVPGSPIFMRLAKQSRHLEVQILLADQYGNNAISIFGRDCSVORRHQKIEEAPAAIATPA 398  
Qy 319 ARESMKAAVRLAKLVGYVSAGTVENLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378  
Db 399 VFEHMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLQVEHPTTEMVADVNL 457  
Qy 379 AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDESSPESFKTQKPKQPOGHVACRIT 438  
Db 458 AAQLQIAMGIPLFRIKDIRMYGVSPWDAPIDFENSA-----HVPCPRGHVIAARIT 510  
Qy 439 AENPDGTGFKPMGALTELNFRSSTSTWGVSVGTSGALHEYADSQGHIFAYGADRSEAR 498  
Db 511 SENPDEGFKPSSGTQVELNFRSNKNVWGYFVAAAGGLHEFADSFQGHCFWSWGENREEAI 570  
Qy 499 KQMVISLKELSIRGDFRTTVEYLIKLLEDAFESNKITTGWLGLIQDRLTAERPAPDLA 558  
Db 571 SNMVVALKELSIKRGDFRTTVEYLIKLLEDAFESQNLNRIIDTGWLDRLIAEKVQAEK 630  
Qy 559 V 559  
Db 631 V 631

RESULT 24  
Q6JIZO MOUSE PRELIMINARY; PRT; 2448 AA.  
AC Q6JIZO;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Acetyl-CoA carboxylase 2.  
GN Name=Acacb;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RA Mao J., Wakil S.J.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451394; AAS13686.1; -; mRNA.  
DR GO; GO:0009343; C:biotin carboxylase complex; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004075; F:biotin carboxylase activity; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR005482; Biotin carb C.  
DR InterPro; IPR000089; Biotin\_lipoYL.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; CphP\_synth\_L\_D2.  
DR InterPro; IPR002114; HPr\_SerP\_S.  
DR Pfam; PF02785; Biotin carb C; 1.  
DR Pfam; PF00364; Biotin\_lipoYL; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP\_GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.  
DR PROSITE; PS50989; COA\_CT\_CTER; 1.  
DR PROSITE; PS50980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
DR PROSITE; PS00589; PTS\_HPR\_SER; UNKNOWN\_1.  
SQ SEQUENCE 2448 AA; 275666 MW; 0B8649F5D2CF1C8A CRC64;

Query Match 61.4%; Score 1783.5; DB 2; Length 2448;  
Best Local Similarity 63.8%; Pred. No. 2.1e-112;  
Matches 346; Conservative 73; Mismatches 108; Indels 15; Gaps 7;

Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
Db 235 ASP-AEFVTRFGGNRVIEKVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPED 293  
Qy 82 LKVNADYIRMAQYVEVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLPES 141  
Db 294 LKANAIEYIKMADQYVPVPGGNNNNYANVELIIDIKRIPIVQAVWAGWGHASENPKLP 353  
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---QG-F 197  
Db 354 LC--KHEIAFLGPPSEAMWALGDKIASTIVAQTLPWSSGLTVEWTEDSRHOGKC 411  
Qy 198 LTVSDDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALV 257  
Db 412 ISVPEDVYEQGCVKVDDEGLQAAEKIGFPLMIKASEGGGKGIRKAESAEDFPMLFRQVQ 471  
Qy 258 GEVPGSPVFMKLAGQARHLEVQILLADQYGNNAISIFGRDCSVORRHQKIEEAPVTIAP 317  
Db 472 SEIPGSPIFLMKLAQNARHLEVQILLADQYGNNAISIFGRDCSVORRHQKIEEAPATIAAP 531  
Qy 318 DARESMKAAVRLAKLVGYVSAGTVENLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377  
Db 532 AVSEFMEQCAVLLAKMVGYSAGTVEYLYS-RDGSFHELNPRLQVEHPTTEMVADVNL 590  
Qy 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDESSPESFKTQKPKQPOGHVACRI 437  
Db 591 PAAQLQIAMGVPLHRLKDIRLLYGESPWG--VTPIPFETPLS-----PPIARGHVIAARI 643  
Qy 438 TAENPDGTGFKPMGALTELNFRSSTSTWGVSVGTSGALHEYADSQGHIFAYGADRSEA 497  
Db 644 TSENPDGFKPSSGTQVELNFRSNKNVWGYFVAAAGGLHEFADSFQGHCFWSWGENREEA 703  
Qy 498 RKQMVISLKELSIRGDFRTTVEYLIKLLEDAFESNKITTGWLGLIQDRLTAERPAPDL 557  
Db 704 ISNMVVALKELSIKRGDFRTTVEYLIKLLEDAFESQNLNRIIDTGWLDRLIAQVQAEK 763  
Qy 558 AV 559



Db 764 GV 765

RESULT 25

Q5SWU9\_MOUSE PRELIMINARY; PRT; 2345 AA.

AC Q5SWU9;

DT 01-FEB-2005 (Tremblrel. 29, Created)

DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE Acetyl-Coenzyme A carboxylase.

GN Name=Acac; ORFNames=RP23-123010.1-001;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Matthews N.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Tracey A.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL596447; CAI25271.1; -; Genomic DNA.

DR EMBL; AL596252; CAI24019.1; -; Genomic DNA.

DR EMBL; AL596252; CAI25271.1; JOINED; Genomic DNA.

DR EMBL; AL596447; CAI24019.1; JOINED; Genomic DNA.

DR GO; GO:0009343; C:biotin carboxylase complex; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0009374; F:biotin binding; IEA.

DR GO; GO:0004075; F:biotin carboxylase activity; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR011761; ATP\_GRASP.

DR InterPro; IPR011764; BC.

DR InterPro; IPR001882; Biotin\_BS.

DR InterPro; IPR005482; Biotin\_carb\_C.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR InterPro; IPR000022; Carboxyl\_trans.

DR InterPro; IPR011763; COA\_CT\_C.

DR InterPro; IPR011762; COA\_CT\_N.

DR InterPro; IPR005481; CPase\_L\_N.

DR InterPro; IPR005479; Cphs synth\_L\_D2.

DR Pfam; PF02785; Biotin\_carb\_C; 1.

DR Pfam; PF00364; Biotin\_lipoyl; 1.

DR Pfam; PF01039; Carboxyl\_trans; 1.

DR Pfam; PF00289; CPase\_L\_chain; 1.

DR Pfam; PF02786; CPase\_L\_D2; 1.

DR PROSITE; PS50975; ATP\_GRASP; 1.

DR PROSITE; PS50979; BC; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.

DR PROSITE; PS50989; COA\_CT\_CTER; 1.

DR PROSITE; PS50980; COA\_CT\_NTER; 1.

DR PROSITE; PS00866; CPASE\_1; 1.

DR PROSITE; PS00867; CPASE\_2; UNKNOWN\_1.

SQ SEQUENCE 2345 AA; 265255 MW; 6995C534B054FE02 CRC64;

Query Match 61.3%; Score 1783; DB 2; Length 2345;

Best Local Similarity 63.6%; Pred. No. 2.1e-112;

Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

Qy 22 ASPVADIRKQGGHSHVITKVLICNNGIAAVKEIRSKWAYETFGDERAIEFTVMATPED 81

Db 102 ASP-AEFTVTRFGGNKVKIEKVLIANNGIAAVKCMRSIRRSYEMFRNERAIRFVVMVTPED 160

Qy 82 LKVNADYTRMADQYVEVPGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141

Db 161 LKANAETIKMADHYVPVPGGPNNNNNYANVELILDIKRIIPQAVWAGWGHASENPKLPED 220

QY 142 LAASKHKLIIFIGPPGSAMRSLGDKISSTIIVAHADVPCMPWPGTGIGIKETMMSD---QGFL 198

Db 221 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSSGLRVDWQENDFSKRIL 278

QY 199 TVSDDVYQACIHTAEGLKAEKIGYPMIKASEGGGKGIRKCTNCEEFKQLYNAVLG 258

Db 279 NVPQDLYEKGYVKDVGDKAAEEVGYPMIKASEGGGKGIRKYNADDFPNLFRQVQA 338

QY 259 EVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVRRHQKIIIEEAPVTIAPED 318

Db 339 EVPGSPVFMRLAKQSRHLEVQILADQYGNNAISIFGRDCSVRRHQKIIIEEAPAAIATPA 398

QY 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP 378

Db 399 VFERMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLOVEHPTTEMVADVNL 457

QY 379 AAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVIDFESSPESFQTKPKPQGHVACRIT 438

Db 458 AAQLQIAMGIPLFRIKDIRMMYGVSPWDAPIDFENSA-----HVPCPRGHVIAARIT 510

QY 439 AENPDGFKPGMGALTELNFRTSTSTWGYFSVGTSGALHEVADSFQGHIFAYGADRSEAR 498

Db 511 SENDEGFKPSSGTQVELNFRTSNKNVWGYFSVAAAGGLHEFADSFQGHCFWSWENREAI 570

QY 499 KQMVSLKELSIKRGDRTTVEYLKLETDAFESNKITTTGWLDELQDLTAERPPADLA 558

Db 571 SNMVVALKELSIKRGDRTTVEYLKLETTESFQNLNRTDGLDLIAEKVQAERPDTMLG 630

QY 559 V 559

Db 631 V 631

RESULT 26

COAL\_HUMAN

ID COAL\_HUMAN STANDARD; PRT; 2346 AA.

AC Q13085;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin

DE carboxylase (EC 6.3.4.14)].

GN Name=ACACA; Synonyms=ACAC, ACC1, ACCA;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=95249602; PubMed=7732023;

RA Abu-Elheiga L., Jayakumar A., Baldini A., Chirala S.S., Wakil S.J.;

RT "Human acetyl-CoA carboxylase: characterization, molecular cloning,

and evidence for two isoforms.";

RL Proc. Natl. Acad. Sci. U.S.A. 92:4011-4015(1995).

RN [2]

RP PHOSPHORYLATION SITE SER-29.

RX PubMed=15302935; DOI=10.1073/pnas.0404720101;

RA Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,

Li J., Cohn M.A., Cantley L.C., Gygi S.P.;

RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";

Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).

CC -!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis

of long-chain fatty acids. This protein carries three functions:

biotin carboxyl carrier protein, biotin carboxylase, and

carboxyltransferase.

CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate

+ malonyl-CoA.

CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

= ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -!- COFACTOR: Biotin.

CC -!- ENZYME REGULATION: By phosphorylation (By similarity).







Db 558 ELSIRGDFRTTVEYLITLLETNRFLDNSIDTAWLDALIAERVQSEKPDILLGV 610

RESULT 28

COAC\_CHICK STANDARD; PRT; 2324 AA.

AC P11029;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin

DE carboxylase (EC 6.3.4.14)].

GN Name=ACAC;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=88139305; PubMed=2893793;

RA Takai T., Yokoyama C., Wada K., Tanabe T.;

RT "Primary structure of chicken liver acetyl-CoA carboxylase deduced

RT from cDNA sequence.";

RL J. Biol. Chem. 263:2651-2657(1988).

RN [2]

RP NUCLEOTIDE SEQUENCE OF 493-820.

RC TISSUE=Liver;

RX MEDLINE=87106011; PubMed=2879745; DOI=10.1016/0014-5793(87)81564-8;

RA Takai T., Wada K., Tanabe T.;

RT "Primary structure of the biotin-binding site of chicken liver acetyl-

RL CoA carboxylase.";

CC FEBS Lett. 212:98-102(1987).

CC -!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis

CC of long-chain fatty acids. This protein carries three functions:

CC biotin carboxyl carrier protein, biotin carboxylase, and

CC carboxyltransferase.

CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate

CC + malonyl-CoA.

CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -!- COFACTOR: Biotin.

CC -!- ENZYME REGULATION: By phosphorylation.

CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)

CC step.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Contains 1 ATP-grasp domain.

CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.

CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.

CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

DR EMBL; J03541; AAA48701.1; -; mRNA.

DR EMBL; X05019; CAA28675.1; -; mRNA.

DR PIR; A29924; A29924.

DR HSSP; Q00955; 1OD4.

DR Ensembl; ENSGALG00000005439; Gallus gallus.

DR InterPro; IPR011761; ATP\_GRASP.

DR InterPro; IPR011764; BC.

DR InterPro; IPR001882; Biotin\_BS.

DR InterPro; IPR005482; Biotin\_carb\_C.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR InterPro; IPR000022; Carboxyl\_trans.

DR InterPro; IPR011763; COA\_CT\_C.

DR InterPro; IPR011762; COA\_CT\_N.

DR InterPro; IPR005481; CPase\_L\_N.

DR InterPro; IPR005479; CPase\_D2\_ATP\_bd.

DR Pfam; PF02785; Biotin\_carb\_C; 1.

DR Pfam; PF00364; Biotin\_lipoyl; 1.

DR Pfam; PF01039; Carboxyl\_trans; 1.

DR Pfam; PF00289; CPSase\_L\_chain; 1.

DR Pfam; PF02786; CPSase\_L\_D2; 1.

DR PROSITE; PS50975; ATP\_GRASP; 1.

DR PROSITE; PS50979; BC; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS50968; BIOTINYL\_LIPOYL; 1.

DR PROSITE; PS50989; COA\_CT\_CTER; 1.

DR PROSITE; PS50980; COA\_CT\_NTER; 1.

DR PROSITE; PS00866; CPSASE\_1; 1.

DR PROSITE; PS00867; CPSASE\_2; 1.

KW ATP-binding; Biotin; Direct protein sequencing;

KW Fatty acid biosynthesis; Ligase; Lipid synthesis;

KW Multifunctional enzyme; Nucleotide-binding; Phosphorylation.

FT DOMAIN 117 618 Biotin carboxylation.

FT DOMAIN 275 466 ATP-grasp.

FT DOMAIN 752 818 Biotinyl/lipoyl.

FT DOMAIN 1675 2171 Carboxyltransferase.

FT NP\_BIND 315 320 ATP (Potential).

FT ACT\_SITE 441 441 By similarity.

FT BINDING 786 786 Biotin (covalent).

FT BINDING 1800 1800 Coenzyme A (By similarity).

FT BINDING 2104 2104 Coenzyme A (By similarity).

FT BINDING 2106 2106 Coenzyme A (By similarity).

FT MOD\_RES 78 78 Phosphoserine (By similarity).

FT MOD\_RES 80 80 Phosphoserine (By similarity).

FT MOD\_RES 1193 1193 Phosphoserine (By similarity).

SQ SEQUENCE 2324 AA; 262720 MW; 3F1C541F01BBBEF6 CRC64;

Query Match 61.2%; Score 1780; DB 1; Length 2324;

Best Local Similarity 63.4%; Pred. No. 3.4e-112;

Matches 343; Conservative 81; Mismatches 103; Indels 14; Gaps 5;

QY 22 ASPVADFIRKQGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81

Db 103 ASP-AEFVTRPFGNVRVIEKVLIANNGIAAVKCMRSIRRSYEMFRNERAIRFVVMVTPED 161

QY 82 LKVNADYIRMDQYVEVPVGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141

Db 162 LKANAERYIKMADHYVPVPGPNNNYANVELILDIAKRIPQAVWAGWGHASENPKLPEL 221

QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSITVAQHADVPVCMPSWGTGIGKETMMSD---QGFL 198

Db 222 L--HKNGIAFMGPPSQAMWALGDKIASIVAQTAGIPTLPWNGSGLRVDWQENDLQKRIL 279

QY 199 TVSDDVYQACIHTABEGLEKAEKIGYPVNIKASEGGGKGIRKCTNGEEFKQLYNAVILG 258

Db 280 NVPQELYEKGYVKDADDGLRAAEVGYPVMIKASEGGGKGIRKVNADDPNLFQVQQA 339

QY 259 EVPGPSFVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEAPVTIAPED 318

Db 340 EVPGPSIFVMRLAKSRHLEVQILADQYGNNAISLFGDRDCSVQRRHQKIIIEAPASIATSV 399

QY 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTEMVSGVNIP 378

Db 400 VFEHMEQCAVKLAKMWGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNL 458

QY 379 AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSSPESFKTQKPKQPOGHVVACRIT 438

Db 459 AAQLQIAMGIPLRIKDIRVMYGVSPWGDGSDIFENSA-----HVCPRGHVIAARIT 511

QY 439 AENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498

Db 512 SENPDEGFKPSSGTVOELNFRSNKNVWGYFSVAAGGLHEFADSQFGHCFSWGENREEAI 571

QY 499 KQMVISLKELSIRGDFRTTVEYLIKLETDAPESNKITTTGWLGDGLIQDRLTAERPPADLA 558

Db 572 SNMVVALKELSIRGDFRTTVEYLIKLETTESFQQNRIDTGWLDRLIAEKVQAEPRDPTMLG 631

QY 559 V 559



Db 309 EYIKMADHYVPVPGGNNNNYANVELIDIALRTQVQAVWAGWGHASENPKLPPELL--HK 366

QY 147 HKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLFTVSDVYQ 206

Db 367 EGLVFLGPPERAMWALGDKVASSIVAQTAEIPTLPWSGSDLKAQYSGKK--IKISSELEFA 424

QY 207 QACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEVPGSPVF 266

Db 425 RGCVTNVEQGLAAVNKIGFPVMIKASEGGGKGIRRVDTTEFPGLFRQVQAEVPGSPIF 484

QY 267 VMKLACQARHLEVQLLADQYGNASISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKA 326

Db 485 VMKLARGARHLEVQLLADQYGNASISLFGDCSIQRRHQKIIIEEAPAIVAQPEVFEDMEKA 544

QY 327 AVRLAKLVGYVSAGTVENWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAM 386

Db 545 AVRLAKMVGYSAGTVELYDPE-GRYFFLELNPRLQVEHPTTEMVADVNLPAQLQIGM 603

QY 387 GIPLYSIDRTLYGMDPRGNEVIDFDSSPESFKTQRPQPGHVACRITAENPDITGF 446

Db 604 GIPLYRLKDIRLLYGESPGSSVIDFE-----NPPNKPSPGHVIAARITSENPDGEF 656

QY 447 KPGMGALTELNFRRSSTWTGWYFSGTSGALHEYADSQFGHIFAYGADRSEARKQWISLK 506

Db 657 KPSSGTVQELNFRSSKNVWGYFSAASGGLHEFADSQFGHCFSGWENRQQAARENVLIALK 716

QY 507 ELSIRGDFRTTVEYLIKLETDAFESNKITTTGWLGLDGLIQRDLTAERPAPDLAV 559

Db 717 ELSIRGDFRTTVEYLIKLETRFLDNSIDTAWLDALIAERVQSEKPDILLGV 769

RESULT 30

Q6JIZI MOUSE PRELIMINARY; PRT; 2345 AA.

AC Q6JIZI;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Acetyl-CoA carboxylase 1.

GN Name=Acaca; Synonyms=Acac;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RA Mao J., Wakil S.J.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY451393; AAS13685.1; -, mRNA.

DR MGI; MGI:108451; Acaca.

DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IMP.

DR InterPro; IPR011761; ATP\_GRASP.

DR InterPro; IPR011764; BC.

DR InterPro; IPR001882; Biotin BS.

DR InterPro; IPR005482; Biotin carb C.

DR InterPro; IPR000089; Biotin\_lipoYL.

DR InterPro; IPR000022; Carboxyl\_trans.

DR InterPro; IPR011763; COA\_CT C.

DR InterPro; IPR011762; COA\_CT N.

DR InterPro; IPR005481; CPase L N.

DR InterPro; IPR005479; CPase D2 ATP\_bd.

DR Pfam; PF02785; Biotin\_carb C; 1.

DR Pfam; PF00364; Biotin\_lipoYL; 1.

DR Pfam; PF01039; Carboxyl\_trans; 1.

DR Pfam; PF00289; CPase L\_chain; 1.

DR Pfam; PF02786; CPase L\_D2; 1.

DR PROSITE; PS50975; ATP\_GRASP; 1.

DR PROSITE; PS50979; BC; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS50968; BIOTINYL LIPOYL; 1.

DR PROSITE; PS50989; COA\_CT\_CTER; 1.

DR PROSITE; PS50980; COA\_CT\_NTER; 1.

DR PROSITE; PS00866; CPSASE 1; 1.

DR PROSITE; PS00867; CPSASE\_2; UNKNOWN 1.

SQ SEQUENCE 2345 AA; 265121 MW; D483B4CECCF6C7D8 CRC64;

Query Match 61.1%; Score 1776; DB 2; Length 2345;

Best Local Similarity 63.4%; Pred. No. 6.4e-112;

Matches 343; Conservative 79; Mismatches 105; Indels 14; Gaps 5;

QY 22 ASPVADFIRKQGGHVSITKVLICNNGIAAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81

Db 102 ASP-AEFVTRFGNKVIEKVLIANNGIAAAVKMRSIRRSYEMFRNERAIRFVVMVTPED 160

QY 82 LKNADYIRMADQYVEVPGGNNNNYANVDLIVDAERAGVHAVWAGWGHASENRLPES 141

Db 161 LKANAIEYIKMADHYVPVPGPPNNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLP 220

QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---QGFL 198

Db 221 LL--KNGIAFMGPPSOAMWALGDKIASSIVAQTAGIPTLPWSGSLRVDWQENDFSKRIL 278

QY 199 TVSDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLG 258

Db 279 NVPQDLYEKGYVKDVEDGLKAAEEVGYPMIKASEGGGKGIRKVNADDFFNLFQVQA 338

QY 259 EVPGPSVFVMKLAGQARHLEVQLLADQYGNASISIFGRDCSVQRRHQKIIIEEAPVTIAPED 318

Db 339 EVPGPSIFVMRLAKQSRHLEVQILADQYGNASISLFGDCSVQRRHQKIIIEEAPAAIATPA 398

QY 319 ARESMEKAAVRLAKLVGYVSAGTVENWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378

Db 399 VFEHMEQCAVKLAKMVGYSAGTVELYLS-QDGSFYFLELNPRLQVEHPTTEMVADVNL 457

QY 379 AAQLQVAMGIPLYSIDRTLYGMDPRGNEVIDFDSSPESFKTQRPQPGHVACRIT 438

Db 458 AAQLQIAMGILPLRIKDIRMYGVSPPWDAPIDFENSA-----HVPCPRGHVIAARIT 510

QY 439 AENPDGTGFKPGMGALTELNFRRSSTWTGWYFSGTSGALHEYADSQFGHIFAYGADRSEAR 498

Db 511 SENPDEGFKPSSGTVQELNFRSNKNVWGYFSAAGGLHEFADSQFGHCFSGWENREEAI 570

QY 499 KOMVISLKELSGRDFRTTVEYLIKLETDAFESNKITTTGWLGLDGLIQRDLTAERPAPDLA 558

Db 571 SNMVVALKELSGRDFRTTVEYLIKLETESFQLNRIDTGWLDRLIAEKVQAGRPTMLG 630

QY 559 V 559

Db 631 V 631

RESULT 31

COAL\_BOVIN

ID COAL\_BOVIN STANDARD; PRT; 2346 AA.

AC Q9TTS3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin

DE carboxylase (EC 6.3.4.14)].

GN Name=ACACA; Synonyms=ACAC, ACCA;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=21378179; PubMed=11485560; DOI=10.1042/0264-6021:3580127;

RA Mao J., Marcos S., Davis S.K., Burzlauff J., Seyfert H.-M.;

RT "Genomic distribution of three promoters of the bovine gene encoding

RT acetyl-CoA carboxylase alpha and evidence that the nutritionally

RT regulated promoter I contains a repressive element different from that



RT in rat.";

RL Biochem. J. 358:127-135(2001).

CC -!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis

CC of long-chain fatty acids. This protein carries three functions:

CC biotin carboxyl carrier protein, biotin carboxylase, and

CC carboxyltransferase (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate

CC + malonyl-CoA.

CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -!- COFACTOR: Biotin.

CC -!- ENZYME REGULATION: By phosphorylation (By similarity).

CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)

CC step.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Contains 1 ATP-grasp domain.

CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.

CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.

CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.

CC -----

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CC removed.

CC -----

CC EMBL; AJ132890; CAB56826.1; -; mRNA.

DR HSSP; Q00955; I0D4.

DR InterPro; IPR011761; ATP GRASP.

DR InterPro; IPR011764; BC\_.

DR InterPro; IPR001882; Biotin BS.

DR InterPro; IPR005482; Biotin carb C.

DR InterPro; IPR000089; Biotin\_lipoYL.

DR InterPro; IPR000022; Carboxyl\_trans.

DR InterPro; IPR011763; COA CT C.

DR InterPro; IPR011762; COA\_CT\_N.

DR InterPro; IPR005481; CPase\_L\_N.

DR InterPro; IPR005479; CPSase\_D2 ATP\_bd.

DR Pfam; PF02785; Biotin carb C; 1.

DR Pfam; PF00364; Biotin\_lipoYL; 1.

DR Pfam; PF01039; Carboxyl\_trans; 1.

DR Pfam; PF00289; CPSase\_L\_chain; 1.

DR Pfam; PF02786; CPSase\_L\_D2; 1.

DR PROSITE; PS0975; ATP GRASP; 1.

DR PROSITE; PS0979; BC; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS0968; BIOTINYL LIPOYL; 1.

DR PROSITE; PS0989; COA\_CT\_CTER; 1.

DR PROSITE; PS0980; COA\_CT\_NTER; 1.

DR PROSITE; PS00866; CPSASE\_1; 1.

DR PROSITE; PS00867; CPSASE\_2; 1.

KW ATP-binding; Biotin; Fatty acid biosynthesis; Ligase; Lipid synthesis;

KW Multifunctional enzyme; Nucleotide-binding; Phosphorylation.

FT DOMAIN 117 618

FT DOMAIN 275 466

FT DOMAIN 752 818

FT NP\_BIND 1698 2194

FT ACT\_SITE 441 441

FT BINDING 786 786

FT BINDING 1823 1823

FT BINDING 2127 2127

FT BINDING 2129 2129

FT MOD\_RES 29 29

FT MOD\_RES 78 78

FT MOD\_RES 80 80

FT MOD\_RES 1201 1201

SQ SEQUENCE 2346 AA; 265303 MW; .32886C5D03EEAE0E CRC64;

Query Match

61.1%; Score 1775; DB 1; Length 2346;

Best Local Similarity 63.7%; Pred. No. 7.5e-112;

Matches 345; Conservative 78; Mismatches 103; Indels 16; Gaps 6;

QY 22 ASPVADFIKQGGHSHVITKVLICNNNGIAAANKVSEIRKWAYETFTGDERAIEFTVMATPED 81

Db 103 ASP-AEFVTRFGGNKVIKVLIANNGIAAANKVSEIRKWAYETFTGDERAIEFTVMATPED 161

QY 82 LKVNADYIRMDADQYVEVPGSGNNNNYANVDLIVDAERAGVHAWAGWGHASENPRLPES 141

Db 162 LKANAETIKWADHYVPVPGGPNNNYANVELILDIKRIPIVQAVWAGWGHASENPKLPEL 221

QY 142 LAASKHKIIFIGPPGSMRSLGKISSTIVAHQADVPCMPWSGTGI----KETMMSDQGF 197

Db 222 LL--XNGIAFMGPPSQAMWALGDKIASSIVAQTAGITPLPWSGSLCVDWHENDFSKR-I 278

QY 198 LTVSDDVYQACIHTAEEGLEKAEKIGYPMWIKASEGGGKGIRKCTNGEEFKQLYNVL 257

Db 279 LNVPELYEKGVKVDVDDGLKAAEEVGYPMWIKASEGGGKGIRKVNADDFFNLFQVQ 338

QY 258 GEVPGSPVFMKLAGQARHLEVLQQLADQYGNASIFGRDCSVQRHKKIIEEAPVTIAPE 317

Db 339 AEVPGSPFVFMRLAKQSRHLEVLQQLADQYGNASIFGRDCSVQRHKKIIEEAPAIATP 398

QY 318 DARESEKAAVRLAKLVGYVSAGTVVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377

Db 399 AVFERMEQCAVKLARVMGYVSAGTVVEYLYS-QDGSFYFLELNPRLQVEHPTTEMVADVNL 457

QY 378 PAAQLQVAMGIPLYISIRDIRTLGYMDPRGNEVIDDFSSPESFKTQKPKQPGHVVACRI 437

Db 458 PAAQLQIAMGIPLYIRIKOIRMYGVSPWGDAPIDFENSA-----HVPKPRGHVIAARI 510

QY 438 TAENPDGTGFKPGMGALTENLNFSSSTSTWGYFSGTSGALHEYADSQGHIFAYGADRSEA 497

Db 511 TSENPDGFKPSSGTQVELNFRSNKNVWGYFSAAGLHEFADSQGHCFSGWGENREA 570

QY 498 RKQMVISLKELSIKIRGDFRTTVEYLIKLETDFAFESNKITTGWLDGLIQDRLTAERPPADL 557

Db 571 ISNMVVALKELSIKIRGDFRTTVEYLIKLETFESQNLNRTGTGWLDRLIAEKVQAEPRDTML 630

QY 558 AV 559

Db 631 GV 632

RESULT 32

COAL SHEEP

ID COAL SHEEP STANDARD; PRT; 2346 AA.

AC Q28559;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin

DE carboxylase (EC 6.3.4.14)].

GN Name=ACACA; Synonyms=ACAC;

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Finn-Dorset; TISSUE=Adipose tissue;

RX MEDLINE=95197015; Pubmed=7890176; DOI=10.1016/0378-1119(94)00871-O;

RA Barber M.C., Travers M.T.;

RT "Cloning and characterisation of multiple acetyl-CoA carboxylase

RT transcripts in ovine adipose tissue.";

RL Gene 154:271-275(1995).

CC -!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis

CC of long-chain fatty acids. This protein carries three functions:

CC biotin carboxyl carrier protein, biotin carboxylase, and

CC carboxyltransferase.

CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate

CC + malonyl-CoA.

CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -!- COFACTOR: Biotin.











DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome 12 SCAF14999, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00029540001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAEE01014999; CAG08536.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
FT NON\_TER 2365 2365  
SQ SEQUENCE 2365 AA; 266780 MW; E8E6297417182246 CRC64;  
  
Query Match 59.0%; Score 1716; DB 2; Length 2365;  
Best Local Similarity 58.9%; Pred. No. 8.1e-108;  
Matches 341; Conservative 73; Mismatches 113; Indels 52; Gaps 8;  
  
QY 22 ASPVADFIRKQGHSHVTK-----VLICNNGIAAVK 52  
DB 28 ASP-AEFVTRFGGTRVIEKVNKPPNHRFFLYQLFLHPSLVALLVLSQVLIANNGLAAVK 86  
  
QY 53 EIRSIRKWAYETFGDERAIEFTVMTAPEDLKVNDYIRMDQYVEVPGGNNNNYANVDL 112  
DB 87 CMRSIRWAYEMFRNERTIRFVMTPTEDLKANAIEYIKMADHYVPVPGPNNNYANVEL 146  
  
QY 113 IVDVAERAGV-----HAWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGD 164  
DB 147 IVDIAKRIPVQVLCSLTFRAVWAGWGHASENPKLPPELL--DKAGISFLGPSSKAMWALGD 204  
  
QY 165 KISSTIVAQAHDVPCMPWPGTGK----ETVMSDQGLTVSDDDVYQACIHTAEGLKA 220  
DB 205 KVASSIVAQASAGIPTLPWSSSLRVDWAEEDROGNIISVPSEVYAKGCVQDIDMGLAGA 264  
  
QY 221 EKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVGLVPGSPFVFMKLAGARHLEVQ 280  
DB 265 BEIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVGLVPGSPFVFMKLAGARHLEVQ 324  
  
QY 281 LLADQYGNASIFGRDCSVORRHQKIEEAPVTIAPEDARESMEKAAVRLAKLVGVYSAG 340  
DB 325 ILADEYGNASIFGRDCSVORRHQKIEEAPVTIAPEDARESMEKAAVRLAKLVGVYSAG 384  
  
QY 341 TVEWLYSPESGEFAFLNPRLOVHEPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDIRTLY 400  
DB 385 TVEYLFSE-EDGRFHFLELNPRLQVHEPCTEMVADVNLPAALQIAMIPLHRIKDIRLLY 443  
  
QY 401 GMDPRGNEVIDDFDSSPESFQTKRQKPOQGHVACRITAENPDGFKPGMGALTTELNFRS 460

Db 444 GEAPWGDIIINFE--DPVCV-----PSPRGHVIAARITSENPDGFKPSSGTVOELNFRS 496  
QY 461 STSTWGVFSVGTSGALHEYADSQGHIFAYGADRSEARKQMVLSLKELSIKELSGDFTTVEY 520  
Db 497 SKNVWGVFSVGTSGALHEYADSQGHIFAYGADRSEARKQMVLSLKELSIKELSGDFTTVEY 556  
QY 521 LIKLETDAPESNKITGTWLDGLIQDRLTAERPPADLAV 559  
Db 557 LIKLETESFRSNEIDTGWLDYLLIAEKVQAEPRDTMLGI 595  
  
RESULT 39  
Q54J08 DICDI  
ID Q54J08 DICDI PRELIMINARY; PRT; 2282 AA.  
AC Q54J08;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Acetyl-CoA carboxylase.  
GN Name=acca; ORFNames=DDB0230067;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AX4;  
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,  
RA Sugchang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,  
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,  
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,  
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,  
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,  
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindbay R.,  
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,  
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,  
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,  
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Tanaka Y.,  
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,  
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,  
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,  
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,  
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,  
RT "The genome of the social amoeba Dictyostelium discoideum";  
RL Nature 0:0-0(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAF101000171; EAL63219.1; -; Genomic DNA.  
SQ SEQUENCE 2282 AA; 256733 MW; BDBEA99629EE1B2B CRC64;  
  
Query Match 58.5%; Score 1699.5; DB 2; Length 2282;  
Best Local Similarity 61.4%; Pred. No. 1e-106;  
Matches 331; Conservative 71; Mismatches 120; Indels 17; Gaps 6;  
  
QY 25 VADFIRKQGHSHVITKVLICNNGIAAVKIEIRSIRKWAYETFGDERAIEFTVMTAPEDLKV 84  
DB 4 INEYIKLGGDKNIEKILIANNGIAAVKAIKRSVRKWAYTNFGNERAIKFWVMATPEDMKA 63  
  
QY 85 NADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHAWAGWGHASENPRLPESLAA 144  
DB 64 NAEYIRMDQILQVPGGNNNNYANVDIIVDAERAGVQAVWAGWGHASENPRLPDLLSK 123  
  
QY 145 SKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWPGTGKIEKTMMSDQGLTVSDDV 204  
DB 124 TETGIVFIFGPPAKAMADLGDKIASTIVAQSARVACVPWSSGLKVDYSECNG---VPSEI 180  
  
QY 205 YQACIHTAEGLKAIEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVGLVPGSP 264  
DB 181 YGRACINSVEARECAQRVGFFPAMIKASEGGGKGIRKVTSMEDLESSFRQVQNEVPGSP 240



QY 265 VFVVKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESME 324  
Db 241 IFFMKLVSNARHLEVOIVADRHGEAISLNGRDCSVQRRHQKIIIEEGPAIAPTTPQVWEEME 300  
QY 325 KAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLEINPRLOVEHPPTTEMVSGVNIIPAAQLQV 384  
Db 301 RAAVRLVKEVGYGAGTVEYLF--EGEYYFLEINPRLOVEHPVTEQITGVNLPATQLQI 358  
QY 385 AMGIPLYSIRDITLYGM---DPRGNEVIDF-DFSSPESFKTQKPKPOGHVVACRITAE 440  
Db 359 AMGIPLHRIPDIRKLYGRTGDDLYGDSMIDLHDF-----TKRNP-PAGHCIAVRITGE 410  
QY 441 NPDTGFKPGMGALTELNFRSSTSTWGYFVSGALHEYADSQFGHIFAYGADRSEARKQ 500  
Db 411 NPDEGFKPTSGQIHETLFTSTPNIWGYFVSGAKGLHEYADSQFGHIFANGATREEARKT 470  
QY 501 MVISLKELSIRGDFRTTVEYLIKLETDAFESNKTITGWLDGLIQDRLTAERPPADLAV 559  
Db 471 IILGLKEISIRGDIRTPVEYIIHLLLESKDFKENHIHTGWLDQLISEKIQTCKKPTMIVV 529  
RESULT 40  
O70151\_RAT PRELIMINARY; PRT; 2456 AA.  
AC O70151; (Tremblrel. 07, Created)  
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Acetyl-CoA carboxylase.  
GN Name=Acacb;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wistar;  
RX MEDLINE=98322122; PubMed=9655932; DOI=10.1016/S0167-4781(98)00060-8;  
RA Abe K., Shinohara Y., Terada H.;  
RT "Isolation and characterization of cDNA encoding rat muscle type  
RT acetyl-CoA carboxylase";  
RL Biochim. Biophys. Acta 1398:347-352(1998).  
DR EMBL; AB004329; BAA25799.1; -; mRNA.  
DR HSSP; Q00955; IOD4.  
DR Ensembl; ENSRNOG00000000658; Rattus norvegicus.  
DR RGD; 620500; Acacb.  
DR GO; GO:0009343; C:biotin carboxylase complex; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004075; F:biotin carboxylase activity; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR011761; ATP\_GRASP.  
DR InterPro; IPR011764; BC.  
DR InterPro; IPR005482; Biotin carb C.  
DR InterPro; IPR000089; Biotin lipoyl.  
DR InterPro; IPR000022; Carboxyl\_trans.  
DR InterPro; IPR011763; COA\_CT\_C.  
DR InterPro; IPR011762; COA\_CT\_N.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR InterPro; IPR005479; Cphs\_synth\_L\_D2.  
DR InterPro; IPR002114; HPr\_SerP\_S.  
DR Pfam; PF02785; Biotin carb C; 1.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
DR Pfam; PF01039; Carboxyl\_trans; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR PROSITE; PS50975; ATP GRASP; 1.  
DR PROSITE; PS50979; BC; 1.  
DR PROSITE; PS50968; BIOTINYL LIPOYL; 1.  
DR PROSITE; PS50989; COA\_CT\_CTER; 1.  
DR PROSITE; PS50980; COA\_CT\_NTER; 1.  
DR PROSITE; PS00866; CPSASE\_1; UNKNOWN\_1.

DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
DR PROSITE; PS00589; PTS\_HPR\_SER; UNKNOWN\_1.  
SQ SEQUENCE 2456 AA; 276098 MW; C1D41AF0BEA38863 CRC64;  
Query Match 57.6%; Score 1673.5; DB 2; Length 2456;  
Best Local Similarity 60.2%; Pred. No. 6.9e-105;  
Matches 327; Conservative 78; Mismatches 121; Indels 17; Gaps 7;  
QY 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVMTATPED 81  
Db 241 ASP-AEFVTRFGGNRVITVLIANNGIAAIVKMRISRRWAYEMFRNERAIRFVVMVTPED 299  
QY 82 LKVNADYIRMAADQYVEVPGGSNNNNYANVDLIVDAERAGVHVAWAGWGHASENPRLPES 141  
Db 300 LKANAEYKMAADPVLVPVPGPNNNNYANVELIIDIAKRIPVQAVWAGWGHASENPKLPEL 359  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHADVPMPWSGTGKETMMSD---QG-F 197  
Db 360 LC--KHGIAFLGPRVRPMLGLGDRLSSTIVAQTLIPTLPWSGSLTVTEWEDSQHQKC 417  
QY 198 LTVSDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIKCTNGEEFKQLYNAVL 257  
Db 418 ISVTEDVYEQGCVRDVDEGLQAAEKVGFPMLIKASEGGGGKGIKQAESEADFFCFFRQVQ 477  
QY 258 GEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVTIAPE 317  
Db 478 SEIPGSPIFLMKLAQNARHLEVQVLADQYGNNAVSLFGRDCSIQRRHQKIIIEEAPANIAAP 537  
QY 318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLEINPRLOVEHPPTTEMVSGVNI 377  
Db 538 AVFEFMEQCAVLLAKTVVYVSAGTVGYLYS-QDGSFHLEINPRLOVEHPCTEMIADVNL 596  
QY 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQKPKQ-PQGHVVACR 436  
Db 597 PAAQLQIAMGVPLHRLKDIRLLYGESPWG-----VTPVSPFETPLSPPIARGHVIAAR 648  
QY 437 ITAENPDGFKPGMGALTELNFRSSTSTWGYFVSGALHEYADSQFGHIFAYGADRSE 496  
Db 649 ITSENDEAFKPSGGTVQELNFRSNKNVWGYFVSAAGGLHEFPISQFGHCFWSWGENQEE 708  
QY 497 ARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKTITGWLDGLIQDRLTAERPPAD 556  
Db 709 AISNMVVALKELSIRGDFRTTVEYLVNLLLETESLQNNDIDITGWLHDHLIAQRVQAEKPDIM 768  
QY 557 LAV 559  
Db 769 LGV 771

Search completed: February 4, 2006, 18:12:51  
Job time : 253 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:25:06 ; Search time 183 Seconds  
(without alignments)  
1276.320 Million cell updates/sec

Title: US-10-633-835-2  
Perfect score: 2907  
Sequence: 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDLTAERPPADLAV 559

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2907	100.0	559	4 US-10-633-835-2	Sequence 2, Appli
2	2885	99.2	554	4 US-10-633-835-22	Sequence 22, Appl
3	2881	99.1	554	4 US-10-633-835-27	Sequence 27, Appl
4	2872	98.8	554	4 US-10-633-835-17	Sequence 17, Appl
5	2857	98.3	549	4 US-10-633-835-23	Sequence 23, Appl
6	2850	98.0	549	4 US-10-633-835-18	Sequence 18, Appl
7	2850	98.0	549	4 US-10-633-835-28	Sequence 28, Appl
8	2808	96.6	539	4 US-10-633-835-24	Sequence 24, Appl
9	2800	96.3	539	4 US-10-633-835-29	Sequence 29, Appl
10	2797	96.2	539	4 US-10-633-835-19	Sequence 19, Appl
11	2751	94.6	529	4 US-10-633-835-25	Sequence 25, Appl
12	2747	94.5	529	4 US-10-633-835-30	Sequence 30, Appl
13	2746	94.5	529	4 US-10-633-835-20	Sequence 20, Appl
14	2703	93.0	519	4 US-10-633-835-26	Sequence 26, Appl
15	2698	92.8	519	4 US-10-633-835-31	Sequence 31, Appl
16	2694	92.7	519	4 US-10-633-835-21	Sequence 21, Appl
17	2163	74.4	571	4 US-10-633-835-53	Sequence 53, Appl
18	2163	74.4	581	4 US-10-633-835-52	Sequence 52, Appl
19	2163	74.4	591	4 US-10-633-835-6	Sequence 6, Appli
20	2139	73.6	2301	4 US-10-369-493-3698	Sequence 3698, Ap
21	2135	73.4	581	4 US-10-633-835-54	Sequence 54, Appl
22	2109	72.5	571	4 US-10-633-835-55	Sequence 55, Appl
23	2079.5	71.5	2241	4 US-10-369-493-2130	Sequence 2130, Ap
24	2074	71.3	521	4 US-10-633-835-64	Sequence 64, Appl
25	2060	70.9	560	4 US-10-633-835-35	Sequence 35, Appl
26	2060	70.9	570	4 US-10-633-835-34	Sequence 34, Appl
27	2060	70.9	575	4 US-10-633-835-33	Sequence 33, Appl

28	2060	70.9	580	4 US-10-633-835-8	Sequence 8, Appli
29	2060	70.9	2233	4 US-10-369-493-1998	Sequence 1998, Ap
30	2058.5	70.8	550	4 US-10-633-835-36	Sequence 36, Appl
31	2054	70.7	580	4 US-10-633-835-32	Sequence 32, Appl
32	2051	70.6	570	4 US-10-633-835-44	Sequence 44, Appl
33	2051	70.6	575	4 US-10-633-835-38	Sequence 38, Appl
34	2051	70.6	575	4 US-10-633-835-43	Sequence 43, Appl
35	2046	70.4	511	4 US-10-633-835-65	Sequence 65, Appl
36	2042.5	70.3	540	4 US-10-633-835-37	Sequence 37, Appl
37	2033	69.9	560	4 US-10-633-835-45	Sequence 45, Appl
38	2033	69.9	570	4 US-10-633-835-39	Sequence 39, Appl
39	2026	69.7	550	4 US-10-633-835-46	Sequence 46, Appl
40	2020	69.5	501	4 US-10-633-835-66	Sequence 66, Appl
41	2009	69.1	540	4 US-10-633-835-47	Sequence 47, Appl
42	2009	69.1	560	4 US-10-633-835-40	Sequence 40, Appl
43	1994.5	68.6	525	4 US-10-633-835-68	Sequence 68, Appl
44	1973	67.9	491	4 US-10-633-835-67	Sequence 67, Appl
45	1967.5	67.7	515	4 US-10-633-835-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1  
US-10-633-835-2  
; Sequence 2, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; PRIOR FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
US-10-633-835-2

Query Match	100.0%	Score 2907;	DB 4;	Length 559;
Best Local Similarity	100.0%;	Pred. No. 3e-254;		
Matches 559;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNNGIAAIVKEIRSIRKW	60	
Db	1	PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNNGIAAIVKEIRSIRKW	60	
Qy	61	AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGSNNNNYANVDLIQVDAERA	120	
Db	61	AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGSNNNNYANVDLIQVDAERA	120	
Qy	121	GVHAVWAGWGCHASENPRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAQAHDVPCM	180	
Db	121	GVHAVWAGWGCHASENPRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAQAHDVPCM	180	
Qy	181	PWSGTGKETMMSDQGLTVDVYQQACIHTAEEGLEKAEKIGYPMIKASEGGGKGI	240	
Db	181	PWSGTGKETMMSDQGLTVDVYQQACIHTAEEGLEKAEKIGYPMIKASEGGGKGI	240	
Qy	241	RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ	300	
Db	241	RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ	300	
Qy	301	RRHQKIIIEAPVTIAPEDARESMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLELNP	360	
Db	301	RRHQKIIIEAPVTIAPEDARESMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLELNP	360	

QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESF 420  
Db 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESF 420  
QY 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYSFVSGTSGALHEYA 480  
Db 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYSFVSGTSGALHEYA 480  
QY 481 DSQFGHIFAYGADRSEARKQMVISLSELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 540  
Db 481 DSQFGHIFAYGADRSEARKQMVISLSELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 540  
QY 541 DGLIQDRLTAERPPADLAV 559  
Db 541 DGLIQDRLTAERPPADLAV 559

RESULT 2  
US-10-633-835-22  
; Sequence 22, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 22  
; LENGTH: 554  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(554)  
; OTHER INFORMATION: C-terminal deleted Ustilago Accase BC domain (AAs 2-555)  
US-10-633-835-22

Query Match 99.2%; Score 2885; DB 4; Length 554;  
Best Local Similarity 100.0%; Pred. No. 2.9e-252;  
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHVSITKVLICNNGIAAAVKEIRSIRKW 60  
Db 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHVSITKVLICNNGIAAAVKEIRSIRKW 60  
QY 61 AYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGGSNNNNYANVDLIYDVAERA 120  
Db 61 AYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGGSNNNNYANVDLIYDVAERA 120  
QY 121 GVHAWGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180  
Db 121 GVHAWGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180  
QY 181 PWSGTGKETMMSDQGLTVSDDDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 240  
Db 181 PWSGTGKETMMSDQGLTVSDDDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 240  
QY 241 RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 241 RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNP 360  
Db 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNP 360

QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESF 420  
Db 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESF 420  
QY 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYSFVSGTSGALHEYA 480  
Db 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYSFVSGTSGALHEYA 480  
QY 481 DSQFGHIFAYGADRSEARKQMVISLSELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 540  
Db 481 DSQFGHIFAYGADRSEARKQMVISLSELSIRGDFRTTVEYLIKLETDAFESNKITTGWL 540  
QY 541 DGLIQDRLTAERPP 554  
Db 541 DGLIQDRLTAERPP 554  
RESULT 3  
US-10-633-835-27  
; Sequence 27, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 554  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(554)  
; OTHER INFORMATION: N- and C-terminal deleted Ustilago Accase BC domain (AAs 4-547)  
US-10-633-835-27

Query Match 99.1%; Score 2881; DB 4; Length 554;  
Best Local Similarity 100.0%; Pred. No. 6.8e-252;  
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHVSITKVLICNNGIAAAVKEIRSIRKW 62  
Db 1 PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHVSITKVLICNNGIAAAVKEIRSIRKW 60  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGGSNNNNYANVDLIYDVAERAGV 122  
Db 61 ETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGGSNNNNYANVDLIYDVAERAGV 120  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 182  
Db 121 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 180  
QY 183 SGTGKETMMSDQGLTVSDDDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 242  
Db 181 SGTGKETMMSDQGLTVSDDDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 240  
QY 243 CTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQR 302  
Db 241 CTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQR 300  
QY 303 HQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNP 362  
Db 301 HQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNP 360  
QY 363 QVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESF 422



Db 361 QVEHPITMVGVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKT 420  
QY 423 QRKPPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADS 482  
Db 421 QRKPPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADS 480  
QY 483 QFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETDAFESNKITTTGWLDDG 542  
Db 481 QFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETDAFESNKITTTGWLDDG 540  
QY 543 LIQDRLTAERPPAD 556  
Db 541 LIQDRLTAERPPAD 554

RESULT 4  
US-10-633-835-17  
; Sequence 17, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 554  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(554)  
; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 7-560)  
US-10-633-835-17

Query Match 98.8%; Score 2872; DB 4; Length 554;  
Best Local Similarity 100.0%; Pred. No. 4.4e-251;  
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 KAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETF 65  
Db 1 KAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETF 60  
QY 66 GDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGSNNNNYANVDLIVDVAERAGHAV 125  
Db 61 GDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGSNNNNYANVDLIVDVAERAGHAV 120  
QY 126 WAGWGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT 185  
Db 121 WAGWGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT 180  
QY 186 GIKETMMSDQGFLTVSDDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 245  
Db 181 GIKETMMSDQGFLTVSDDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 240  
QY 246 GEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOK 305  
Db 241 GEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOK 300  
QY 306 IIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVE 365  
Db 301 IIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVE 360  
QY 366 HPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQK 425

Db 361 HPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQK 420  
QY 426 PQPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFG 485  
Db 421 PQPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFG 480  
QY 486 HIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETDAFESNKITTTGWLDDGLIQ 545  
Db 481 HIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETDAFESNKITTTGWLDDGLIQ 540  
QY 546 DRLTAERPPADLAV 559  
Db 541 DRLTAERPPADLAV 554

RESULT 5  
US-10-633-835-23  
; Sequence 23, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(549)  
; OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs 2-550)  
US-10-633-835-23

Query Match 98.3%; Score 2857; DB 4; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1e-249;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAVKEIRSIRKW 60  
Db 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAVKEIRSIRKW 60  
QY 61 AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGSNNNNYANVDLIVDVAERA 120  
Db 61 AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGSNNNNYANVDLIVDVAERA 120  
QY 121 GVHAVWAGWGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180  
Db 121 GVHAVWAGWGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180  
QY 181 PWSGTGIKETMMSDQGFLTVSDDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGKI 240  
Db 181 PWSGTGIKETMMSDQGFLTVSDDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGKI 240  
QY 241 RKCTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 241 RKCTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
QY 301 RRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 301 RRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420  
Db 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420

Qy 421 KTQKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGALHEYA 480  
Db 421 KTQKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGALHEYA 480  
Qy 481 DSQFGHIFAYGADRSEARKQMVISLKELSIKELSDFTTVEYLKLETDAFESNKITTWGL 540  
Db 481 DSQFGHIFAYGADRSEARKQMVISLKELSIKELSDFTTVEYLKLETDAFESNKITTWGL 540  
Qy 541 DGLIQDRLT 549  
Db 541 DGLIQDRLT 549

RESULT 6  
US-10-633-835-18  
; Sequence 18, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(549)  
; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 12-560)  
US-10-633-835-18

Query Match 98.0%; Score 2850; DB 4; Length 549;  
Best Local Similarity 100.0%; Pred. No. 4.3e-249;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 FIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERA 70  
Db 1 FIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERA 60  
Qy 71 IEFTVMTATPEDLKNADYIARMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAWGW 130  
Db 61 IEFTVMTATPEDLKNADYIARMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAWGW 120  
Qy 131 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGIKET 190  
Db 121 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGIKET 180  
Qy 191 MMSDQGLTVSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEETF 250  
Db 181 MMSDQGLTVSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEETF 240  
Qy 251 QLYNAVILGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRHQQIIEEA 310  
Db 241 QLYNAVILGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRHQQIIEEA 300  
Qy 311 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPITE 370  
Db 301 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPITE 360  
Qy 371 MVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESFQTKPQOG 430  
Db 361 MVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESFQTKPQOG 420

Qy 431 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGALHEYADSQFGHIFAY 490  
Db 421 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGALHEYADSQFGHIFAY 480  
Qy 491 GADRSEARKQMVISLKELSIKELSDFTTVEYLKLETDAFESNKITTWGLDGLIQDRLTA 550  
Db 481 GADRSEARKQMVISLKELSIKELSDFTTVEYLKLETDAFESNKITTWGLDGLIQDRLTA 540  
Qy 551 ERPPADLAV 559  
Db 541 ERPPADLAV 549  
RESULT 7  
US-10-633-835-28  
; Sequence 28, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 28  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(549)  
; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 7-555)  
US-10-633-835-28

Query Match 98.0%; Score 2850; DB 4; Length 549;  
Best Local Similarity 100.0%; Pred. No. 4.3e-249;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 KAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETF 65  
Db 1 KAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETF 60  
Qy 66 GDERAIEFTVMTATPEDLKNADYIARMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAV 125  
Db 61 GDERAIEFTVMTATPEDLKNADYIARMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAV 120  
Qy 126 WAGWGHAENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGT 185  
Db 121 WAGWGHAENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGT 180  
Qy 186 GIKETMMSDQGLTVSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 245  
Db 181 GIKETMMSDQGLTVSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 240  
Qy 246 GEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRHQQ 305  
Db 241 GEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRHQQ 300  
Qy 306 IIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVE 365  
Db 301 IIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVE 360  
Qy 366 HPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESFQTKRQ 425  
Db 361 HPTTEMVSGVNIIPAAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDFDFSSPESFQTKRQ 420  
Qy 426 PQQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGALHEYADSQFG 485

Db 421 POQGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFG 480  
Qy 486 HIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITGWLDGLIQ 545  
Db 481 HIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITGWLDGLIQ 540  
Qy 546 DRLTAERPP 554  
Db 541 DRLTAERPP 549

RESULT 8  
US-10-633-835-24  
; Sequence 24, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(539)  
; OTHER INFORMATION: C-terminal deleted Ustilago Accase BC domain (AAs 2-540)  
US-10-633-835-24

Query Match 96.6%; Score 2808; DB 4; Length 539;  
Best Local Similarity 100.0%; Pred. No. 2.7e-245;  
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKW 60  
Db 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKW 60  
Qy 61 AYETFGDERAIEFTVMATPEDLKVNDYIYRMADQYVEVPGGNNNNYANVDLIVDVAERA 120  
Db 61 AYETFGDERAIEFTVMATPEDLKVNDYIYRMADQYVEVPGGNNNNYANVDLIVDVAERA 120  
Qy 121 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180  
Db 121 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180  
Qy 181 PWSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240  
Db 181 PWSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240  
Qy 241 RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 241 RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Qy 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Qy 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFESSPESF 420  
Db 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFESSPESF 420  
Qy 421 KTQKPPQGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480

Db 421 KTQKPPQGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Qy 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITGW 539  
Db 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITGW 539  
RESULT 9  
US-10-633-835-29  
; Sequence 29, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(539)  
; OTHER INFORMATION: N- and C-terminal deleted Ustilago Accase BC domain (AAs 12-550)  
US-10-633-835-29

Query Match 96.3%; Score 2800; DB 4; Length 539;  
Best Local Similarity 100.0%; Pred. No. 1.4e-244;  
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 FIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKWYETFGDERA 70  
Db 1 FIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKWYETFGDERA 60  
Qy 71 IEFTVMATPEDLKVNDYIYRMADQYVEVPGGNNNNYANVDLIVDVAERAGVHAVWAGWG 130  
Db 61 IEFTVMATPEDLKVNDYIYRMADQYVEVPGGNNNNYANVDLIVDVAERAGVHAVWAGWG 120  
Qy 131 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKET 190  
Db 121 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKET 180  
Qy 191 MMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKIRKCTNGEEFK 250  
Db 181 MMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKIRKCTNGEEFK 240  
Qy 251 QLYNAVLEVPSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEA 310  
Db 241 QLYNAVLEVPSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEA 300  
Qy 311 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTE 370  
Db 301 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTE 360  
Qy 371 MVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFESSPESFKTKRKPQPG 430  
Db 361 MVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFESSPESFKTKRKPQPG 420  
Qy 431 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY 490  
Db 421 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY 480  
Qy 491 GADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITGWLDGLIQDRLT 549  
Db 481 GADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITGWLDGLIQDRLT 539



RESULT 10  
US-10-633-835-19  
; Sequence 19, Application US/106333835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(539)  
; OTHER INFORMATION: N-terminal deleted Ustilago ACCse BC domain (AAs 22-560)  
US-10-633-835-19

Query Match 96.2%; Score 2797; DB 4; Length 539;  
Best Local Similarity 100.0%; Pred. No. 2.7e-244;  
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 PASPVADFIRKQGGHSHVITKVLICNNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPE 80  
DB 1 PASPVADFIRKQGGHSHVITKVLICNNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPE 60  
QY 81 DLKVNADYIRMADQYVEVPGGNNNNYANVDLIVDVAERAGVHAWAGWGHASENPRLPE 140  
DB 61 DLKVNADYIRMADQYVEVPGGNNNNYANVDLIVDVAERAGVHAWAGWGHASENPRLPE 120  
QY 141 SLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLTV 200  
DB 121 SLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLTV 180  
QY 201 SDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKOLYNVNLGEV 260  
DB 181 SDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKOLYNVNLGEV 240  
QY 261 PGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSVQRRHQKIIIEAPVTIAPEDAR 320  
DB 241 PGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSVQRRHQKIIIEAPVTIAPEDAR 300  
QY 321 ESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAA 380  
DB 301 ESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAA 360  
QY 381 QLQVAMGIPLYSIRDITLYGMDPRGNEVIDEFSSESFKTKQKPPQGHVACRITAE 440  
DB 361 QLQVAMGIPLYSIRDITLYGMDPRGNEVIDEFSSESFKTKQKPPQGHVACRITAE 420  
QY 441 NPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEYADSFQGHIFAYGADRSEARKQ 500  
DB 421 NPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEYADSFQGHIFAYGADRSEARKQ 480  
QY 501 MVISLKELSGRDFRTTVEYLIKLETDAPESNKITTTGLDGLIQDRRLTAERPPADLAV 559  
DB 481 MVISLKELSGRDFRTTVEYLIKLETDAPESNKITTTGLDGLIQDRRLTAERPPADLAV 539

RESULT 11  
US-10-633-835-25  
; Sequence 25, Application US/106333835

; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Ustilago maydis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(529)  
; OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs 2-530)  
US-10-633-835-25

Query Match 94.6%; Score 2751; DB 4; Length 529;  
Best Local Similarity 100.0%; Pred. No. 3.9e-240;  
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNNGIAAVKEIRSIRKW 60  
DB 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNNGIAAVKEIRSIRKW 60  
QY 61 AYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGNNNNYANVDLIVDVAERA 120  
DB 61 AYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGNNNNYANVDLIVDVAERA 120  
QY 121 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180  
DB 121 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180  
QY 181 PWSGTGKETMMSDQGLTVSDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGKI 240  
DB 181 PWSGTGKETMMSDQGLTVSDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGKI 240  
QY 241 RKCTNGEEFKOLYNVNLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSVQ 300  
DB 241 RKCTNGEEFKOLYNVNLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSVQ 300  
QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
DB 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDEFSSESF 420  
DB 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDEFSSESF 420  
QY 421 KTQRKPPQGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEYA 480  
DB 421 KTQRKPPQGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEYA 480  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSGRDFRTTVEYLIKLETTDA 529  
DB 481 DSQFGHIFAYGADRSEARKQMVISLKELSGRDFRTTVEYLIKLETTDA 529

RESULT 12  
US-10-633-835-30  
; Sequence 30, Application US/106333835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.

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; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(529)
; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)
US-10-633-835-30

Query Match      94.5%; Score 2747; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 9e-240;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 PLETAPASPVADFIRKQGHSHVITKVLICNNGIAAIVKAEIRSIKWAYETFGDERAIEFTV 75
Db 1 PLETAPASPVADFIRKQGHSHVITKVLICNNGIAAIVKAEIRSIKWAYETFGDERAIEFTV 60

QY 76 MATPEDLKVNADYIRMAQYVEVPVGGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASEN 135
Db 61 MATPEDLKVNADYIRMAQYVEVPVGGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASEN 120

QY 136 PRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPWSGTGKETMMSDQ 195
Db 121 PRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPWSGTGKETMMSDQ 180

QY 196 GFLTVDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNA 255
Db 181 GFLTVDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNA 240

QY 256 VLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIA 315
Db 241 VLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIA 300

QY 316 PEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGV 375
Db 301 PEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGV 360

QY 376 NIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFSSPESFQTKRKPQGHVVAC 435
Db 361 NIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFSSPESFQTKRKPQGHVVAC 420

QY 436 RITAENPDGTGFKPGMGALTENLFRSSTSTWGYSFGTSGALHEYADSQFGHIFAYGADRS 495
Db 421 RITAENPDGTGFKPGMGALTENLFRSSTSTWGYSFGTSGALHEYADSQFGHIFAYGADRS 480

QY 496 EARKQMVISLKELSIKRGDFRTTVEYLIKLETDAPESNKITTGWLDGLI 544
Db 481 EARKQMVISLKELSIKRGDFRTTVEYLIKLETDAPESNKITTGWLDGLI 529

RESULT 13
US-10-633-835-20
; Sequence 20, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
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; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(529)
; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)
US-10-633-835-20

Query Match      94.5%; Score 2746; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 KQGGHSHVITKVLICNNGIAAIVKAEIRSIKWAYETFGDERAIEFTVMTATPEDLKVNADYIR 90
Db 1 KQGGHSHVITKVLICNNGIAAIVKAEIRSIKWAYETFGDERAIEFTVMTATPEDLKVNADYIR 60

QY 91 MADQYVEVPVGGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKII 150
Db 61 MADQYVEVPVGGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKII 120

QY 151 FIGPPGSAMRSLGDKISSITIVAQHADVPCMPWSGTGKETMMSDQGLTIVSDVYQQACI 210
Db 121 FIGPPGSAMRSLGDKISSITIVAQHADVPCMPWSGTGKETMMSDQGLTIVSDVYQQACI 180

QY 211 HTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLEVPVGVFVMKL 270
Db 181 HTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLEVPVGVFVMKL 240

QY 271 AGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAPEDARESMEKAAVRL 330
Db 241 AGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAPEDARESMEKAAVRL 300

QY 331 AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIAPAAQLQVAMGIPL 390
Db 301 AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIAPAAQLQVAMGIPL 360

QY 391 YSIRDITLYGMDPRGNEVIDFSSPESFQTKRKPQGHVVACRITAENPDGTGFKPGM 450
Db 361 YSIRDITLYGMDPRGNEVIDFSSPESFQTKRKPQGHVVACRITAENPDGTGFKPGM 420

QY 451 GALTENLFRSSTSTWGYSFGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSI 510
Db 421 GALTENLFRSSTSTWGYSFGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSI 480

QY 511 RGDFTTVEYLIKLETDAPESNKITTGWLDGLIQDRLTAERPPADLAV 559
Db 481 RGDFTTVEYLIKLETDAPESNKITTGWLDGLIQDRLTAERPPADLAV 529

RESULT 14
US-10-633-835-26
; Sequence 26, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
```

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; LENGTH: 519
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(519)
; OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs2-520)
US-10-633-835-26

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Query Match	93.0%;	Score 2703;	DB 4;	Length 519;
Best Local Similarity	100.0%;	Pred. No. 8.5e-236;		
Matches 519;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAVKEIRSIRKW	60	
DB	1	PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAVKEIRSIRKW	60	
QY	61	AYETFGDERAIEFTVMATPEDLKNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA	120	
DB	61	AYETFGDERAIEFTVMATPEDLKNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA	120	
QY	121	GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM	180	
DB	121	GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM	180	
QY	181	PWSTGIGIKETWMSDQGFLLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI	240	
DB	181	PWSTGIGIKETWMSDQGFLLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI	240	
QY	241	RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQ	300	
DB	241	RKCTNGEEFKQLYNALVGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQ	300	
QY	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP	360	
DB	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP	360	
QY	361	RLQVEHPTTEMVSGVNIPTAAQLQVAMGIPLYISIRDIRTLTYGMDPRGNEVIDDFSSPESF	420	
DB	361	RLQVEHPTTEMVSGVNIPTAAQLQVAMGIPLYISIRDIRTLTYGMDPRGNEVIDDFSSPESF	420	
QY	421	KTQRKPQPGHVHVACRITAENPDTGFKPGMGALTTELNFRSSTTWGYFSVGTSGALHEYA	480	
DB	421	KTQRKPQPGHVHVACRITAENPDTGFKPGMGALTTELNFRSSTTWGYFSVGTSGALHEYA	480	
QY	481	DSQFGHIFAYGADRSEARKQWISLKELSIRGDFRTTVE	519	
DB	481	DSQFGHIFAYGADRSEARKQWISLKELSIRGDFRTTVE	519	

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RESULT 15
US-10-633-835-31
; Sequence 31, Application US/10633835
; Publication NO. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE

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; LOCATION: (1)...(519)
; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAS 22-540)
US-10-6333-835-31

Query Match      92.8%; Score 2698; DB 4; Length 519;
Best Local Similarity 100.0%; Pred. No. 2.4e-235;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PASPVADFIKQGGHSHVITKVLICNNGIAAAKEIRSIRKWAYETFGDERAIEFTVMATPE 80
Db 1 PASPVADFIKQGGHSHVITKVLICNNGIAAAKEIRSIRKWAYETFGDERAIEFTVMATPE 60

QY 81 DLKVNADYIRMAQQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHAHENRPLPE 140
Db 61 DLKVNADYIRMAQQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHAHENRPLPE 120

QY 141 SLAASKHKIIFIGPPGSAMRSIGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGFITV 200
Db 121 SLAASKHKIIFIGPPGSAMRSIGDKISSTIVAQAHDVPCMPWSGTGIKETMMSDQGFITV 180

QY 201 SDDVYQQACIHTAEEGLEKAKEKIGYPVMIKASEGGGGKIRKCTNGEEFKQLYNALVGEV 260
Db 181 SDDVYQQACIHTAEEGLEKAKEKIGYPVMIKASEGGGGKIRKCTNGEEFKQLYNALVGEV 240

QY 261 PGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHOKIIEEAPVTIIAPEDAR 320
Db 241 PGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHOKIIEEAPVTIIAPEDAR 300

QY 321 ESMEKAAVRLAKLVGYVSAGTVWEWLYSPESGEFAFLELNPRQLQVEHPTTEMVSGVNI PAA 380
Db 301 ESMEKAAVRLAKLVGYVSAGTVWEWLYSPESGEFAFLELNPRQLQVEHPTTEMVSGVNI PAA 360

QY 381 QLQVAMGIPLYISIRDIRTLYGMDPRGNEVIDDFSPSPESFKTQRKPPQGHVVACRITAE 440
Db 361 QLQVAMGIPLYISIRDIRTLYGMDPRGNEVIDDFSPSPESFKTQRKPPQGHVVACRITAE 420

QY 441 NPDTGFKPGMGALTELNFRSSTSTWGYFVSVTSGALHEYADSQFGHIFAYGADRSEARKQ 500
Db 421 NPDTGFKPGMGALTELNFRSSTSTWGYFVSVTSGALHEYADSQFGHIFAYGADRSEARKQ 480

QY 501 MVISLKELSIRGDFRTTVEYLIKLETDAFESNKIITGW 539
Db 481 MVISLKELSIRGDFRTTVEYLIKLETDAFESNKIITGW 519

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RESULT 16
US-10-633-835-21
; Sequence 21, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(519)
; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 42-560)
US-10-633-835-21

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QY 65 FGDERAIEFTVMATPEDLVNADYIRMDQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124  
Db 87 FGDERAIQFTVMATPEDLVNADYIRMDHYVEVPGGTNNNNYANVELIVDVAERNVHA 146  
QY 125 VWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSG 184  
Db 147 VWAGWGHASENPKLPESLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQAQVPCIPWSG 206  
QY 185 TGIKETMMSDQGFELTVSDDDVYQACIHTAEGLKAEKIGYPMIKASEGGGKGIRKCT 244  
Db 207 TGVDVAVQIDKKGIQVTVDDDTYAKGCVTSWQEGLEKARQIGFPMIKASEGGGKGIRKAV 266  
QY 245 NGEFPKQLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQ 304  
Db 267 SEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNNAISIFGRDCSVQRRHQ 326  
QY 305 KIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364  
Db 327 KIIEEAPVTIAKPDTFKAMEEAAVRLGLVGYVSAGTVEWLYSHADDKFFYLELNPRLQV 386  
QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTOR 424  
Db 387 EHPTTEGVSGVNLPAASQLQIAMGIPLHRISDIRLLYGVDPKLSIDEIDFKNPDSEKTOR 446  
QY 425 KPQPOGHVVACRITAENPDGTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSOF 484  
Db 447 RPSKPGHLTACRITSEDPGEGFKPSNGVMHNLFRSSSNVWGYFSVGTGGIHSFSDSO 506  
QY 485 GHIFAYGADRSEARKQMVISLKELSIKELSGIRGDFRTTVEYLIKLETDAPESNKITTTGWLDEL 544  
Db 507 GHIFAYGENRSASRKHVMVIALKELSGIRGDFRTTVEYLIKLETEAFEENTITTTGWLDEL 566  
QY 545 QDRLTAERPPADLAV 559  
Db 567 SKKLTAEPRDPKMLAV 581  
RESULT 19  
US-10-633-835-6  
; Sequence 6, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Ellich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; TYPE: PRT  
; LENGTH: 591  
; ORGANISM: Magnaporthe grisea  
US-10-633-835-6

Query Match 74.4%; Score 2163; DB 4; Length 591;  
Best Local Similarity 73.5%; Pred. No. 9.9e-187;  
Matches 408; Conservative 59; Mismatches 88; Indels 0; Gaps 0;

QY 5 HKAVSQFIGGNPLETAPASPVADPIRKQGGHVSITKVLICNNGIAAIAVKEIRSIRKWAYET 64  
Db 37 HKIADHFIGGNRLNENAPPSKVKEVAAHDGHTVITNVLIANNGIAAIAVKEIRSIRKWAYET 96  
QY 65 FGDERAIEFTVMATPEDLVNADYIRMDQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124  
Db 97 FGDERAIQFTVMATPEDLVNADYIRMDHYVEVPGGTNNNNYANVELIVDVAERNVHA 156

QY 125 VWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSG 184  
Db 157 VWAGWGHASENPKLPESLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQAQVPCIPWSG 216  
QY 185 TGIKETMMSDQGFELTVSDDDVYQACIHTAEGLKAEKIGYPMIKASEGGGKGIRKCT 244  
Db 217 TGVDVAVQIDKKGIQVTVDDDTYAKGCVTSWQEGLEKARQIGFPMIKASEGGGKGIRKAV 276  
QY 245 NGEFPKQLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQ 304  
Db 277 SEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNNAISIFGRDCSVQRRHQ 336  
QY 305 KIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364  
Db 337 KIIEEAPVTIAKPDTFKAMEEAAVRLGLVGYVSAGTVEYLYSHADDKFFYLELNPRLQV 396  
QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTOR 424  
Db 397 EHPTTEGVSGVNLPAASQLQIAMGIPLHRISDIRLLYGVDPKLSIDEIDFKNPDSEKTOR 456  
QY 425 KPQPOGHVVACRITAENPDGTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSOF 484  
Db 457 RPSKPGHLTACRITSEDPGEGFKPSNGVMHNLFRSSSNVWGYFSVGTGGIHSFSDSO 516  
QY 485 GHIFAYGADRSEARKQMVISLKELSIKELSGIRGDFRTTVEYLIKLETDAPESNKITTTGWLDEL 544  
Db 517 GHIFAYGENRSASRKHVMVIALKELSGIRGDFRTTVEYLIKLETEAFEENTITTTGWLDEL 576  
QY 545 QDRLTAERPPADLAV 559  
Db 577 SKKLTAEPRDPKMLAV 591

RESULT 20  
US-10-369-493-3698  
; Sequence 3698, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 3698  
; LENGTH: 2301  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(2301)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-3698

Query Match 73.6%; Score 2139; DB 4; Length 2301;  
Best Local Similarity .68.8%; Pred. No. 1.2e-183;  
Matches 411; Conservative 58; Mismatches 86; Indels 42; Gaps 2;

QY 5 HKAVSQFIGGNPLETAPASPVADPIRKQGGHVSIT-----KVLI 43  
Db 6 HNLAPHFIGGNRLNENAPPSKVKEVAAHDGHTVITNVRFLALPAVQTRFXHLLVFOVLI 65  
QY 44 CNNGIAAIAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLVNADYIRMDQYVEVPGGSN 103  
Db 66 ANNGIAAIAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLVNADYIRMDHYVEVPGGTN 125





Db 157 VWAGWGHAENPKLPESLAASPKKIIIFIGPPGSAMRSLGDKISSTIVAQAQVPCIPWSG 216

Qy 185 TGIKETWMSDQFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCT 244

Db 217 TGVDVQIDKKGIIVTDDTYAKGCVTSWQEGLEKARQIGFPPVMIKASEGGGKGIRKAV 276

Qy 245 NGEFQQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRHQ 304

Db 277 SEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNNAISIFGRDCSVQRHQ 336

Qy 305 KIIIEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOV 364

Db 337 KIIIEAPVTIAPKPTTFKAMEEAAVRLGLRVLGYVSAGTVEYLYSHADDKFYFLELNPRLOV 396

Qy 365 EHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTOR 424

Db 397 EHPTTEGVSGVNLPAQQLIAMGIPHLHRISDIRLLYGVDPKLSVEIDDFKNPDSEKTOR 456

Qy 425 KPQPOGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSOF 484

Db 457 RPSKPGHLTACRITSEDPGEGFKPSNGVMHNLNFRSSNVWGYFSVGTGGIHSFSDSO 516

Qy 485 GHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLYKLLETDAFESNKITGW 539

Db 517 GHIFAYGENRSASRKHVMIALKELSIRGDFRTTVEYLYKLLETDAFEENTITGW 571

RESULT 23

US-10-369-493-2130

; Sequence 2130, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 2130

; LENGTH: 2241

; TYPE: PRT

; ORGANISM: Schizosaccharomyces pombe

US-10-369-493-2130

Query Match 71.5%; Score 2079.5; DB 4; Length 2241;

Best Local Similarity 71.4%; Pred. No. 2.9e-178;

Matches 394; Conservative 62; Mismatches 95; Indels 1; Gaps 1;

Qy 9 SQFIGGNPLETAPASPVDPIRQKGGHVSITKVLICNNGIAAIVKEIRSKWAYETFGDE 68

Db 1 NHILGNSLDKAPAGKVQDYASHGGHTVITSILIANNGIAAIVKEIRSKWAYETFNE 60

Qy 69 RAIEFTVMATPDLKVNADYIRMADQYVEVPGSGNNNNYANVDLIVDVAERAGVHAVWAG 128

Db 61 RAIKFTVMATPDDLKVNADYIRMADQYVEVPGSGNNNNYANVELIVDIAERMNVHAVWAG 120

Qy 129 WGHASENPRLPESLAASKHKIIIFIGPPGSAMRSLGDKISSTIVAQAHADVPCMPWSGTGK 188

Db 121 WGHASENPKLPPEMLSSASSKKIVIFIGPPGSAMRSLGDKISSTIVAQAARVPCMSWSGNEL 180

Qy 189 ETWMSDQ-GFLTVDVDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGE 247

Db 181 QVRIDEETNIVTDDVYQACIRSAEAGIAEAKIGYPVMIKASEGGGKGIRQVTSTE 240

Qy 248 EFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRHQKII 307

Db 241 KFAQAFQOVLDELPGSPVFMKLAGQARHLEVQILADQYGNNAISIFGRDCSVQRHQKII 300

Qy 308 EEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHP 367

Db 301 EEAPVTIAPATTFHEMERAARVLGELVGYASAGTIEYLYEPENDRFFYLELNPRLOVEHP 360

Qy 368 TTEMVSGVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTORKPQ 427

Db 361 TTEMVSGVNLPAQQLQVAMGLPLSRIPHIRELYGLPRDGDSEIDFFFNQNPESFKVKVPT 420

Qy 428 PQGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHI 487

Db 421 PKGHCVACRITSEDPGEGFKPSSGMIKOLNFRSSSNVWGYFSVGTAGGHEFADSQFGHI 480

Qy 488 PAYGADRSEARKQMVISLKELSIRGDFRTTVEYLYKLLETDAFESNKITTTGWLDDGLIQDR 547

Db 481 FSFAESRESSRKSMMVALKELSIRGDFRTTVEYLYVRLLETKEFSENEFTTGWLDRLIAQK 540

Qy 548 LTAERPPADLAV 559

Db 541 VTSARPDKMLAV 552

RESULT 24

US-10-633-835-64

; Sequence 64, Application US/10633835

; Publication No. US20040086994A1

; GENERAL INFORMATION:

; APPLICANT: Elich, Tedd D.

; APPLICANT: Volrath, Sandra L.

; APPLICANT: Weatherly, Stephanie C.

; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF

; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS

; FILE REFERENCE: 9280.2

; CURRENT APPLICATION NUMBER: US/10/633,835

; CURRENT FILING DATE: 2003-08-04

; PRIOR APPLICATION NUMBER: US 60/401,170

; PRIOR FILING DATE: 2003-08-05

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 64

; LENGTH: 521

; TYPE: PRT

; ORGANISM: Magnaporthe grisea

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(521)

; OTHER INFORMATION: N-terminal deleted Magnaporthe ACCase BC domain (AAs 72-592)

US-10-633-835-64

Query Match 71.3%; Score 2074; DB 4; Length 521;

Best Local Similarity 75.0%; Pred. No. 9.6e-179;

Matches 391; Conservative 55; Mismatches 75; Indels 0; Gaps 0;

Qy 39 TKVLICNNGIAAIVKEIRSKWAYETFGDERAIEFTVMATPDLKVNADYIRMADQYVEV 98

Db 1 TNVLIANNGIAAIVKEIRSVRKWAYETFGDERAIQFTVMATPDLQANADYIRMADHYVEV 60

Qy 99 PGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIIFIGPPGSA 158

Db 61 PGGTNNNNYANVELIVDVAERMNVHAVWAGWGHASENPKLPESLAASPKKIIIFIGPPGSA 120

Qy 159 MRSGLDKISSTIVAQAHADVPCMPWSGTGKETMMSDQGLTVSDDVYQQACIHTAEEGLE 218

Db 121 MRSGLDKISSTIVAQAHAQVPCIPWSGTGVDVAQIDKKGIIVTDDDTYAKGCVTSWQEGLE 180

Qy 219 KAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLE 278

Db 181 KARQIGFPPVMIKASEGGGKGIRKAVSEEGFEELYKAAASEIPGSPIFIMKLAGNARHLE 240

Qy 279 VQLLADQYGNNAISIFGRDCSVQRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGYVS 338

Db 241 VQLLADQYGNNAISIFGRDCSVQRHQKIIIEAPVTIAPEDTFKAMEEAAVRLGLRVLGYVS 300

QY	339	AGTVEWLYSPESGEFAFLELNPRLQVEHPITTEMVSGVNI	PAAQLOVAMGIPLYSIRD	398
Db	301	AGTVEYLYSHADDKFYFLELNPRLQVEHPITTEGVSGVNL	PASQLQIAMGIPLHRISDIRL	360
QY	399	LYGMDPRGNEVIDDFSSPESFKTORKPQPOGHVVACRITAEN	PDTFGFKPGMGALTELNF	458
Db	361	LYGVDPKLSTEIDDFDKNPDSEKTORRPPSPKGHLTACRIT	SEDDPGEFGFKPSNGVMHELNF	420
QY	459	RSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARK	QOMVISLKELSI	518
Db	421	RSSSNVWGYFSVGTQGGIHSFSDSQFGHIFAYGENRSASR	KHMVIALKELSI	480
QY	519	EYLIKLETDAPESNKITTTGWLDDGLIQDRLTAERPPADLAV	559	
Db	481	EYLIKLETEAFEENTITTTGWLDELISKLTAERPDKMLAV	521	

```

RESULT 25
US-10-633-835-35
; Sequence 35, Application US/10633835
; Publication No., US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elith, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(560)
; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAS
; OTHER INFORMATION: 22-581)
US-10-633-835-35

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QY	361	RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVIDDFDSSPESF	420
Dd	362	RLQVEHPTTEMVSGVNLPAALQIAMGIPMHRISDITRTLYGWNPHSASEIDFEFKTQDAT	421
QY	421	KTQRKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA	480
Dd	422	KKQRRPIPKGHCTACRITSEDPNDGDFKPSGGTLHELNFRSSSNVWGYFSVGNNGNIHSFS	481
QY	481	DSQFGHIFAYGADRSEARKQMWISLKELSIRGDFRRTTVEYLIKLETDAFESNKITTTGWL	540
Dd	482	DSQFGHIFAFGENROASRKHMMVVALKELSIRGDFRRTTVEYLIKLETDATEDNTITTTGWL	541
QY	541	DGLIQDRLTAERPPADLAV	559
Dd	542	DDLITTKMTAEKPDPTLAV	560

RESULT 26  
 US-10-633-835-34  
 ; Sequence 34, Application US/10633835  
 ; Publication No. US20040086994A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elich, Tedd D.  
 ; APPLICANT: Volrath, Sandra L.  
 ; APPLICANT: Weatherly, Stephanie C.  
 ; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
 ; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
 ; FILE REFERENCE: 9280.2  
 ; CURRENT APPLICATION NUMBER: US/10/633,835  
 ; CURRENT FILING DATE: 2003-08-04  
 ; PRIOR APPLICATION NUMBER: US 60/401,170  
 ; PRIOR FILING DATE: 2003-08-05  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 34  
 ; LENGTH: 570  
 ; TYPE: PRT  
 ; ORGANISM: Saccharomyces cerevisiae  
 ; FEATURE:  
 ; NAME/KEY: MISC FEATURE  
 ; LOCATION: (1)..(570)  
 ; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (P  
 ; OTHER INFORMATION: 12-581)  
 US-10-633-835-34

Query Match	70.9%	Score 2060;	DB 4;	Length 560;
Best Local Similarity	69.1%	Pred. No. 2e-177;		
Matches 386;	Conservative 76;	Mismatches 89;	Indels 8;	Gaps 3;
QY	3	PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAAAVKEIRSIRKWAY	62	
Db	8	PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAAVKEIRSIRKWAY	62	
QY	63	ETFGDERAIEFTVMATPEDLKVNNADIYRMADQYVEVPGGSNNNNYANVVDLIVDVAERAGV	122	
Db	63	ETFGDDRTQFVAMATPEDLEANAHEYIRMADQYIEVPGGTNNNNYANVVDLIVDIAERADV	122	
QY	123	HAVWAGWGCHASENPRLPESLAASKHKIIFIGPPGSAMRSIGDKISSTIVAQHADVPVCPWP	182	
Db	123	DAVWAGWGCHASENPLLPEKLSQSKRKVIFIGPPGNAMFSLGDKISSTIVAQSAKVPCIPW	182	
QY	183	SGTGIKETMMSDQ--GFLTVDSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI	240	
Db	183	SGTGV-DTVHVEKTLVSVDDDIYQKGCCTSPEDGLQAKRIGFPPVMIKASEGGGKGI	241	
QY	241	RKCTNGEEFKQLYNAVLGEVPGSPVFMKLAGQARHLEVLQLLADQYGNIAISIFGRDCSVQ	300	
Db	242	RQVEREEDFIALYHQAAINEIPGSPIFIMKLAGRARHLEVLQLLADQYGTNISLFGDCSVQ	301	
QY	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP	360	
Db	302	RRHQKIIIEAPVTIAKAETFHEMEKAAVRLKLVGYVSAGTVEYLYSHDDGKFYFLELNP	361	

Query Match	70.9%;	Score	2060;	DB	4;	Length	570;
Best Local Similarity	69.1%;	Pred. No.	2e-177;				
Matches	386;	Conservative	76;	Mismatches	89;	Indels	8;
Gaps	3;						
Qy	3	PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSHVITKVLICNNGIAA	KEIRSIRKWAY	62			
Db	18	PGH-----FIGLNTVDKLEESPLRDFVKXSHGHTVISKILIANNGIAA	KEIRSVRKWAY	72			
Qy	63	ETFGDERAIEFTVMATPEDLKVNDYIRMDAQYVEVPGSSNNNNYANVDL	IVDVAERAGV	122			
Db	73	ETFGDRTVQFVAMATPEDLEANAEYIRMDAQYIEVPGGTNNNNYANVDL	IVDIAERADV	132			
Qy	123	HAVWAGWGCHASENPRLPESLAASKHIIIFIGPPGSAMRSLGDKISSTIV	AQHADVPCMPW	182			
Db	133	DAVWAGWGCHASENPLLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSTIV	AQSAKVPCIPW	192			
Qy	183	SGTGKETMMSDQ--GFLTVDVYQQACIHTAEEGLEKAEKIGYPVMIKASE	GGGGKGI	240			
Db	193	SGTGV-DTVHVDKTLGVSDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASE	GGGGKGI	251			
Qy	241	RKCTNGEEFKQLYNVLTGEVPGSPVFMKLAGQARHLEVQLLADQYGN	NAISIFGRDCSVQ	300			
Db	252	QVREBEDFIALYHQAAEIPGSPIFIMKLAGRARHLEVQLLADQYGT	NISLFGRDCSVQ	311			
Qy	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTV	EWLYSPESGEFAFLNLP	360			
Db	312	RRHOKIIIEAPVTIAKAEFTHEMEKAARVIGKIVGYVSAGTV	EYVYSHDDGKVEYETLNP	371			

QY	361	RLQVEHPPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITRTLYGMDPGRNEVIDPFDSSPESF	420
Dd	372	RLQVEHPPTTEMVSGVNLPAAQQLIAMGIPMHRISDITRTLYGMNPHSASEIDFEFKTQDAT	431
QY	421	KTORKKPOQGHVVACRITAENPDGTGFKPCMGALTELNFRSSTWTGYFSVGTS GALHEYA	480
Dd	432	KKQRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGYFSVGNNGNIHSFS	491
QY	481	DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETDAFESNKITTGWL	540
Dd	492	DSQFGHIFAPGENROASRKHMVVALKELSIRGDFRTTVEYLKLETFEDNTITTWGL	551
QY	541	DGLIQDRLLTAERPPPADLAV	559
Dd	552	DDLITHMTAEKPPDPTLAV	570

RESULT 27  
 US-10-633-835-33  
 ; Sequence 33, Application US/10633835  
 ; Publication No. US20040086994A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elich, Tedd D.  
 ; APPLICANT: Volrath, Sandra L.  
 ; APPLICANT: Weatherly, Stephanie C.  
 ; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
 ; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
 ; FILE REFERENCE: 9280.2  
 ; CURRENT APPLICATION NUMBER: US/10/633,835  
 ; CURRENT FILING DATE: 2003-08-04  
 ; PRIOR APPLICATION NUMBER: US 60/401,170  
 ; PRIOR FILING DATE: 2003-08-05  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 33  
 ; LENGTH: 575  
 ; TYPE: PRT  
 ; ORGANISM: Saccharomyces cerevisiae  
 ; FEATURE:  
 ; NAME/KEY: MISC FEATURE  
 ; LOCATION: (1)..(575)  
 ; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain  
 ; OTHER INFORMATION: 7-581)  
 US-10-633-835-33

Query Match	70.9%;	Score 2060;	DB 4;	Length 575;
.Best Local Similarity	69.1%;	Pred. No. 2.le-177;		
Matches 386;	Conservative	76;	Mismatches 89;	Indels 8; Gaps 3;
QY	3	PDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSIRKWAY	62	
DB	23	PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSVRKWAY	77	
QY	63	ETFGDERAIEFTVMATPEDLKVNDAYIRMADQYVEVPGGSNNNNYANVDLIVDAERAGV	122	
DB	78	ETFGDDRTVQFVAMATPEDLEANAERYIRMADQYIEVPGGTNNNNYANVDLIVDIAERADV	137	
QY	123	HAVWAGWCHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW	182	
DB	138	DAVWAGWCHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVAQSAKVPCIPW	197	
QY	183	SGTGIKETMSDQ--GFLTVDVYQQACIHTAEEGLEKAEEKIGYPVMIKASEGGGKGI	240	
DB	198	SGTGV-DTVHVDEKTLGLSVDDDIYQKGCCTSPEDGLQAKAKRIGFPVMIKASEGGGKGI	256	
QY	241	RKCTNGEFPKQLYNAVLGVEPSPVFMKLAGQARHLEVQLLADQYNAISIFGRDCSVQ	300	
DB	257	RQVEREEDFIALYHQAAANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGRDSCSVQ	316	
QY	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVSEWLYSPESGEFAFLELNP	360	
DB	317	RRHQKIIIEAPVTIAKATFEHEMEKAAVRLKLVGYVSAGTVEYLYSHDDGKFFYLELNP	376	

RESULT 28  
US-10-633-835-8  
; Sequence 8, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Ellich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 580  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-633-835-8

	Query Match	70.9%;	Score 2060;	DB 4;	Length 580;
	Best Local Similarity	69.1%;	Pred. No. 2.1e-177;		
	Matches 386;	Conservative	76;	Mismatches 89;	Indels 8; Gaps 3;
QY	3	PDHKAVSOFIGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAVKEIRSIRKWAY	62		
DB	28	PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSIRKWAY	82		
QY	63'	ETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSSNNNNYANVDLIVDVAERAGV	122		
DB	83	ETFGDDRTVQFVAMATPEDLEANAERYIRMADQYIEVPGGTNNNNYANVDLIVDIAERADV	142		
QY	123	HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPW	182		
DB	143	DAVWAGWGHASENPLLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSITIVAQSAKVPCIPW	202		
QY	183	SGTGKETWMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYVPMIKASEGGGKGI	240		
DB	203	SGTGV-DTVHVEKDTGLVSVDDDIYQKCGCTSPEDGLQAKRIGFPVPMIKASEGGGKGI	261		
QY	241	RKCTNGEFPQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNATISIFGRDCSVQ	300		
DB	262	RQVEREEDFIALYHQAAEIPGSPIFIMKLAGRARHLEVQLLADQYGTNLSIFGRDCSVQ	321		
QY	301	RRHQKITEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP	360		
DB	322	RRHQKITEAPVTIAKAETTFHEMEKAAVRLGKLVGYVSAGTVEYLYSHDDGKFYFLELNP	381		
QY	361	RLQVEHPPTMVGWNIPAAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVTDFFSSPESF	420		
DB	382	RLQVEHPPTMVGWNIPAAQLQIAMGIPMHRISDITRTLYGMNPHSASEIDFEKTDQAT	441		



QY 421 KTQRKPQGHVAVACRITAENPDGPKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 442 KKQRRPPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSNVWGYFSVGNNGNIHSFS 501  
QY 481 DSQFGHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLKLETTAFESNKITTTGWL 540  
Db 502 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLKLETTAFEDNITTTGWL 561  
QY 541 DGLIQDRLTAERPPADLAV 559  
Db 562 DDLITHKMTAEKPDPTLAV 580  
RESULT 29  
US-10-369-493-1998  
; Sequence 1998, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 1998  
; LENGTH: 2233  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-1998

Query Match 70.9%; Score 2060; DB 4; Length 2233;  
Best Local Similarity 69.1%; Pred. No. 1.7e-176;  
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;  
QY 3 PDHKAVSQFIGNPLETAPASPVADFIRKQGHVSITKVLICNNGIAAVKEIRSIRKWAY 62  
Db 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 83  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGV 122  
Db 84 ETFGDDRTVQFVAMATPEDLEANAIEYIRMDQYIEVPGGNNNNYANVDLIVDAERADV 143  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPW 182  
Db 144 DAVWAGWGHASENPLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSITIVAQSAKVPCIPW 203  
QY 183 SGTGIKETMMSDQ--GFLTVDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 240  
Db 204 SGTGV-DTVHDEKTLVSVDDDIYQKGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGI 262  
QY 241 RKCTNGEEFKQLYNALVEVPSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300  
Db 263 QOVEREEEDFIALYHQAAEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGRDCSVQ 322  
QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 323 RRHQKIIIEAPVTIAKAETTHEMEKAAVRLKLVGYVSAGTVEYLYSHDDGKFYFLELNP 382  
QY 361 RLQVEHPTTEMVSGVNI PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFESSPESF 420  
Db 383 RLQVEHPTTEMVSGVNL PAAQLQIAMGIPMHRISDITLYGNPHSASEIDFEFTQDAT 442  
QY 421 KTQRKPQGHVAVACRITAENPDGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 443 KKQRRPPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSNVWGYFSVGNNGNIHSFS 502

QY 481 DSQFGHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLKLETTAFESNKITTTGWL 540  
Db 503 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLKLETTAFEDNITTTGWL 562  
QY 541 DGLIQDRLTAERPPADLAV 559  
Db 563 DDLITHKMTAEKPDPTLAV 581  
RESULT 30  
US-10-633-835-36  
; Sequence 36, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36  
; LENGTH: 550  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(550)  
; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A  
; OTHER INFORMATION: 32-581  
US-10-633-835-36

Query Match 70.8%; Score 2058.5; DB 4; Length 550;  
Best Local Similarity 69.7%; Pred. No. 2.6e-177;  
Matches 384; Conservative 76; Mismatches 88; Indels 3; Gaps 2;  
QY 11 FIGGNPLETAPASPVADFIRKQGHVSITKVLICNNGIAAVKEIRSIRKWAYETFGDERA 70  
Db 1 FIGLNTVDKLEESPLRDFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAYETFGDDRT 60  
QY 71 IEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHAVWAGW 130  
Db 61 VQFVAMATPEDLEANAIEYIRMDQYIEVPGGNNNNYANVDLIVDAERADVDAVWAGW 120  
QY 131 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPWSGTGIKET 190  
Db 121 HASENPLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSITIVAQSAKVPCIPWSGTGV-DT 179  
QY 191 MMSDQ--GFLTVDVYQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIKCTNGEE 248  
Db 180 VHDEKTLVSVDDDIYQKGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGIQVEREED 239  
QY 249 FKQLYNALVEVPSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIE 308  
Db 240 FIALYHQAAEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGRDCSVQRRHQKIIIE 299  
QY 309 EAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPT 368  
Db 300 EAPVTIAKAETTHEMEKAAVRLKLVGYVSAGTVEYLYSHDDGKFYFLELNPRLQVEHPT 359  
QY 369 TEMVSGVNI PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFESSPESFQTKRPQ 428  
Db 360 TEMVSGVNL PAAQLQIAMGIPMHRISDITLYGNPHSASEIDFEFTQDATKKQRRPIP 419  
QY 429 QGHVVACRITAENPDGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIF 488  
Db 420 KGHCTACRITSEDPNDGFKPSGGTLHELNFRSSNVWGYFSVGNNGNIHSFSDSQFGHIF 479



Db 497 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLKLETFEDFEDNTITTTGWL 556  
Qy 541 DGLIQDRLTAERP 553  
Db 557 DDLITHKMTAEKP 569

RESULT 33  
US-10-633-835-38  
; Sequence 38, Application US/106333835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(575)  
; OTHER INFORMATION: C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAS  
; OTHER INFORMATION: 2-576)  
US-10-633-835-38

Query Match 70.6%; Score 2051; DB 4; Length 575;  
Best Local Similarity 69.3%; Pred. No. 1.4e-176;  
Matches 383; Conservative 76; Mismatches 86; Indels 8; Gaps 3;

Qy 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSIRKWAY 62  
Db 28 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSIRKWAY 82  
Qy 63 ETFGDERAIEFTVMATPEDLKVNADYIRMDQYIEVPGGSSNNNNYANVDLIVDVAERAGV 122  
Db 83 ETFGDDRTVQFVAMATPEDLEANAIEYIRMDQYIEVPGGTTNNNNYANVDLIVDIAERADV 142  
Qy 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW 182  
Db 143 DAVWAGWGHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVAQSAKVPCIPW 202  
Qy 183 SGTGIKETMMSDQ--GFLTVDSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGKI 240  
Db 203 SGTGV-DTVHVDEKTLGLSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGKI 261  
Qy 241 RKCTNGEEFKQLYNALVEVPVGMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 262 RQVEREEDFIALYHQAANEIPGSPIFIMKLAGARHLEVQLLADQYGTNLSLFGRDCSVQ 321  
Qy 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 322 RRHQKIIIEAPVTIAKAETTHEMEKAAVRLGLVGYVSAGTVEYLYSHDDGKFYFLELNP 381  
Qy 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSSPESF 420  
Db 382 RLQVEHPTTEMVSGVNLPAALQIAMIPIHMRISDITLYGMNPHSASEIDFEFTQDAT 441  
Qy 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 442 KKQRRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGYFSVGNNGNIHSFS 501  
Qy 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETFDAFESNKITTTGWL 540

Db 502 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLKLETFEDFEDNTITTTGWL 561  
Qy 541 DGLIQDRLTAERP 553  
Db 562 DDLITHKMTAEKP 574

RESULT 34  
US-10-633-835-43  
; Sequence 43, Application US/106333835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(575)  
; OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC  
; OTHER INFORMATION: domain (AAS 4-578)  
US-10-633-835-43

Query Match 70.6%; Score 2051; DB 4; Length 575;  
Best Local Similarity 69.3%; Pred. No. 1.4e-176;  
Matches 383; Conservative 76; Mismatches 86; Indels 8; Gaps 3;

Qy 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSIRKWAY 62  
Db 26 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSIRKWAY 80  
Qy 63 ETFGDERAIEFTVMATPEDLKVNADYIRMDQYIEVPGGSSNNNNYANVDLIVDVAERAGV 122  
Db 81 ETFGDDRTVQFVAMATPEDLEANAIEYIRMDQYIEVPGGTTNNNNYANVDLIVDIAERADV 140  
Qy 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW 182  
Db 141 DAVWAGWGHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVAQSAKVPCIPW 200  
Qy 183 SGTGIKETMMSDQ--GFLTVDSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGKI 240  
Db 201 SGTGV-DTVHVDEKTLGLSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGKI 259  
Qy 241 RKCTNGEEFKQLYNALVEVPVGMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 260 RQVEREEDFIALYHQAANEIPGSPIFIMKLAGARHLEVQLLADQYGTNLSLFGRDCSVQ 319  
Qy 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 320 RRHQKIIIEAPVTIAKAETTHEMEKAAVRLGLVGYVSAGTVEYLYSHDDGKFYFLELNP 379  
Qy 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSSPESF 420  
Db 380 RLQVEHPTTEMVSGVNLPAALQIAMIPIHMRISDITLYGMNPHSASEIDFEFTQDAT 439  
Qy 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 440 KKQRRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGYFSVGNNGNIHSFS 499  
Qy 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLKLETFDAFESNKITTTGWL 540



Db	500	DSQFCHIFAFGENRQASRKHMVVALKELSRGDFRTTVEYLIKLETFEDFEDNTITGWL	559
QY	541	DGLIQDRLTAERP	553
Db	560	DDLITHKMTAERP	572

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RESULT 35
US-10-633-835-65
; Sequence 65, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(511)
; OTHER INFORMATION: N- and C-terminal deleted Magnaporthe ACCase BC domain (AAS
; OTHER INFORMATION: 72-582)
US-10-633-835-65

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Db 481 EYLKLETEAFEENTTTGWLDLISKLT 511

RESULT 36
US-10-633-835-37
; Sequence 37, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Eich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(540)
; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A
; OTHER INFORMATION: 42-581)
US-10-633-835-37

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519 EYLIKLETAFAESNKITTGWLDGLIODRLT 549

RESULT 37  
US-10-633-835-45  
; Sequence 45, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(560)  
; OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC  
; OTHER INFORMATION: domain (AAs 12-571)  
US-10-633-835-45

Query Match 69.9%; Score 2033; DB 4; Length 560;  
Best Local Similarity 69.2%; Pred. No. 5.6e-175;  
Matches 380; Conservative 75; Mismatches 86; Indels 8; Gaps 3;  
  
QY 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAA VKEIRSIRKWAY 62  
Db 18 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAA VKEIRSIRKWAY 72  
  
QY 63 ETFGDERAIEFTVMATPEDLKVADYIRMDQYVEVPGGSNNNNYANVDLIVDAERAGV 122  
Db 73 ETFGDDRTVQFVAMATPEDLEANA EYIRMDQYIEVPGGTNNNNYANVDLIVDAERADV 132  
  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPW 182  
Db 133 DAVWAGWGHASENPLLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSITIVAQSAKVPCIPW 192  
  
QY 183 SGTGIKETMMSDQ--GFLTVDVYQACIHTAEGLEKAEKIGYPMVMIKASEGGGKGI 240  
Db 193 SGTGV-DTVHVDEKTLVSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 251  
  
QY 241 RKCTNGEEFKQLYNAVLEVPVGMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 252 QVREEDFIALYHQAA NEIPGSPIFIMKLAGRARHLEVQLLADQYGTNLSLFGDCSVQ 311  
  
QY 301 RRHQKIIIEEAPVTIAPEDARESMEEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 312 RRHQKIIIEEAPVTIAKAETHEMEKAAVRLGLVGYVSAGTVEYLYSHDDGKFYFLELNP 371  
  
QY 361 RLQVEHPTTEMVSGVNI PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420  
Db 372 RLQVEHPTTEMVSGVNL PAAQLQIAMGIPMHRISDITLYGMNPHSASEIDFEFTQDAT 431  
  
QY 421 KTQKKPQPGHVHVACRITAENPDGTGFKPGMGALTTELNFRSSTSTWGFVSGTSGALHEYA 480  
Db 432 KKQRRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGFVSGVNGNIHSFS 491  
  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETFDAFESNKITTGWL 540  
Db 492 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLIKLETFEDFEDNTITTGWL 551  
  
QY 541 DGLIQDRLT 549  
Db 552 DDLITHKMT 560

RESULT 38  
US-10-633-835-39  
; Sequence 39, Application US/10633835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39  
; LENGTH: 570  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(570)  
; OTHER INFORMATION: C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A  
; OTHER INFORMATION: 2-571)  
US-10-633-835-39

Query Match 69.9%; Score 2033; DB 4; Length 570;  
Best Local Similarity 69.2%; Pred. No. 5.7e-175;  
Matches 380; Conservative 75; Mismatches 86; Indels 8; Gaps 3;  
  
QY 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAA VKEIRSIRKWAY 62  
Db 28 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAA VKEIRSIRKWAY 82  
  
QY 63 ETFGDERAIEFTVMATPEDLKVADYIRMDQYVEVPGGSNNNNYANVDLIVDAERAGV 122  
Db 83 ETFGDDRTVQFVAMATPEDLEANA EYIRMDQYIEVPGGTNNNNYANVDLIVDAERADV 142  
  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPW 182  
Db 143 DAVWAGWGHASENPLLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSITIVAQSAKVPCIPW 202  
  
QY 183 SGTGIKETMMSDQ--GFLTVDVYQACIHTAEGLEKAEKIGYPMVMIKASEGGGKGI 240  
Db 203 SGTGV-DTVHVDEKTLVSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 261  
  
QY 241 RKCTNGEEFKQLYNAVLEVPVGMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 262 QVREEDFIALYHQAA NEIPGSPIFIMKLAGRARHLEVQLLADQYGTNLSLFGDCSVQ 321  
  
QY 301 RRHQKIIIEEAPVTIAPEDARESMEEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 322 RRHQKIIIEEAPVTIAKAETHEMEKAAVRLGLVGYVSAGTVEYLYSHDDGKFYFLELNP 381  
  
QY 361 RLQVEHPTTEMVSGVNI PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420  
Db 382 RLQVEHPTTEMVSGVNL PAAQLQIAMGIPMHRISDITLYGMNPHSASEIDFEFTQDAT 441  
  
QY 421 KTQKKPQPGHVHVACRITAENPDGTGFKPGMGALTTELNFRSSTSTWGFVSGTSGALHEYA 480  
Db 442 KKQRRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGFVSGVNGNIHSFS 501  
  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETFDAFESNKITTGWL 540  
Db 502 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLIKLETFEDFEDNTITTGWL 561  
  
QY 541 DGLIQDRLT 549  
Db 562 DDLITHKMT 570

RESULT 39  
US-10-633-835-46  
; Sequence 46, Application US/106333835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 46  
; LENGTH: 550  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(550)  
; OTHER INFORMATION: N- and C-terminal deleted  
; OTHER INFORMATION: domain (AAs 17-566)  
US-10-633-835-46

Query Match 69.7%; Score 2026; DB 4; Length 550;  
Best Local Similarity 69.7%; Pred. No. 2.3e-174;  
Matches 379; Conservative 73; Mismatches 84; Indels 8; Gaps 3;  
QY 3 PDHKAQSVQFIGGNPLETAPASPVADFIKQGGHVSIVTKVLICNNGIAAIAVKEIRSIRKWAY 62  
Db .13 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIAVKEIRSIRKWAY 67  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPVGGSSNNNNYANVDLIVDVAERAGV 122  
Db 68 ETFGDRTVQFVAMATPEDLEANAIEYIRMAQYIEVPVGGTNNNNYANVDLIVDIAERADV 127  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQAHDVPCMPW 182  
Db 128 DAVWAGWGHASENPLLPKLSQSKRKVIFIGPPGNMRSLGDKISSITIVAQAQAKVPCIPW 187  
QY 183 SGTGIKETMMSDQ--GFLTVDVYQQAACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 240  
Db 188 SGTGV-DTVHVEKDTGLVSDVDIYQKGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGI 246  
QY 241 RKTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSVQ 300  
Db 247 RQVEREEDFIALYHQAANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGDCSVQ 306  
QY 301 RRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 307 RRHOKIIEEAPVTIAKAETFEHEKAAVRLGLVGYVSAGTVEYLYSHDDGKFYFLELNP 366  
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFESSPESF 420  
Db 367 RLQVEHPTTEMVSGVNLPAALQIAMGIPMHRISDITLYGMNPHSASEIDFEEKTQDAT 426  
QY 421 KTQKPKPOQGHVVACRITAENPDGFKPGMGALTELNFSSSTWGYFSGVTSGALHEYA 480  
Db 427 KKQRRPIPKGHCTACRITSEDNDGFKPSGGTTLHELNFSSSNVWGYFSGVNGNIIHFS 486  
QY 481 DSQFGHIPAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLETAFAESNKITTGWL 540  
Db 487 DSQFGHIFAFGENRQASRKHMVMVALKELSIRGDFRTTVEYLIKLETAFAEDNTITTTGWL 546

QY 541 DGLI 544  
Db 547 DDLI 550

Search completed: February 4, 2006, 18:28:37  
Job time : 187 secs

RESULT 40  
US-10-633-835-66  
; Sequence 66, Application US/106333835  
; Publication No. US20040086994A1  
; GENERAL INFORMATION:  
; APPLICANT: Elich, Tedd D.  
; APPLICANT: Volrath, Sandra L.  
; APPLICANT: Weatherly, Stephanie C.  
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF  
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS  
; FILE REFERENCE: 9280.2  
; CURRENT APPLICATION NUMBER: US/10/633,835  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US 60/401,170  
; PRIOR FILING DATE: 2003-08-05  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 66  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: N- and C-terminal deleted  
; OTHER INFORMATION: Magnaporthe ACCase BC domain (AAs  
US-10-633-835-66

Query Match 69.5%; Score 2020; DB 4; Length 501;  
Best Local Similarity 75.4%; Pred. No. 7.1e-174;  
Matches 378; Conservative 54; Mismatches 69; Indels 0; Gaps 0;  
QY 39 TKVLICNNGIAAIAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEV 98  
Db 1 TNVLIANNGIAAIAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLQANADYIRMAQYVEV 60  
QY 99 PGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSA 158  
Db 61 PGGTNNNNYANVELIVDVAERMNVHAVWAGWGHASENPKLPESLAASPKIIFIGPPGSA 120  
QY 159 MRLSGDKISSITIVAQAHDVPCMPWSGTGKETMMSDQGLFTVSDVYQQAACIHTAEEGLE 218  
Db 121 MRLSGDKISSITIVAQAQVPCIPWSGTGVDVAVQIDKKGIVTVDDDTYAKGCVTSWQEGLE 180  
QY 219 KAEKIGYPVMIKASEGGGKGIKCTNGEERFKQLYNVAVLGEVPGSPVFMKLAGQARHLE 278  
Db 181 KARQIGFPVMIKASEGGGKGIKAVSEEGFEELYKAAASEIPGSPIFIMKLAGNARHLE 240  
QY 279 VQLLADQYGNASISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVS 338  
Db 241 VQLLADQYGNISLFGDCSVQRRHQKIIIEEAPVTIAKPDFTFKAMEEAAVRLGRLVGYVS 300  
QY 339 AGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDIT 398  
Db 301 AGTVEYLYSHADDKFYFLELNPRLQVEHPTTEGVSGVNLPAALQIAMGIPLHRISDIRL 360  
QY 399 LYGMDPRGNEVIDDFESSPESFKTQKPOQGHVVACRITAENPDGFKPGMGALTELNF 458  
Db 361 LYGVDPKLSLEIDDFEKNPDSEKTRRRSPKGHLTACRITSEDGEGFKPSNGVMHELNF 420  
QY 459 RSSSTWGYFSGVTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTV 518  
Db 421 RSSSNVWGYFSGVTQGGIHSFSDSQFGHIFAYGENRSASRKHMVIALKELSIRGDFRTTV 480  
QY 519 EYLIKLETAFAESNKITTGW 539  
Db 481 EYLIKLETAFAEENTITTGW 501



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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:25:41 ; Search time 16 Seconds  
(without alignments)  
409.400 Million cell updates/sec

Title: US-10-633-835-2  
Perfect score: 2907  
Sequence: 1 PPDHKAVSQFIGGNPLETA.....LDGLIQRLTAERPPADLAV 559

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1777.5	61.1	2455	7 US-11-186-999-14	Sequence 14, Appl
2	1777.5	61.1	2455	7 US-11-186-999-16	Sequence 16, Appl
3	1769.5	60.9	2256	7 US-11-144-368-4	Sequence 4, Appl
4	1769.5	60.9	2458	7 US-11-186-999-13	Sequence 13, Appl
5	1766.5	60.8	2458	7 US-11-186-999-6	Sequence 6, Appl
6	1739	59.8	2455	7 US-11-186-999-4	Sequence 4, Appl
7	1693.5	58.3	2458	7 US-11-186-999-11	Sequence 11, Appl
8	1673.5	57.6	2456	7 US-11-186-999-8	Sequence 8, Appl
9	1673.5	57.6	2456	7 US-11-186-999-10	Sequence 10, Appl
10	1669.5	57.4	2483	7 US-11-186-999-2	Sequence 2, Appl
11	1591.5	54.7	1096	6 US-10-995-561-710	Sequence 710, App
12	666	22.9	453	6 US-10-467-657-1642	Sequence 1642, Ap
13	640.5	22.0	703	6 US-10-821-234-1317	Sequence 1317, Ap
14	625	21.5	1151	6 US-10-793-626-2448	Sequence 2448, Ap
15	572	19.7	1124	6 US-10-858-730-12	Sequence 12, Appl
16	568	19.5	1127	6 US-10-858-730-13	Sequence 13, Appl
17	543.5	18.7	1140	6 US-10-858-730-208	Sequence 208, App
18	512.5	17.6	341	6 US-10-793-626-218	Sequence 218, App
19	508.5	17.5	453	6 US-10-793-626-804	Sequence 804, App
20	487	16.8	309	6 US-10-793-626-648	Sequence 648, App
21	178	6.1	1071	6 US-10-467-657-1654	Sequence 1654, Ap
22	167	5.7	1066	7 US-11-055-822-370	Sequence 370, App
23	167	5.7	1066	7 US-11-055-822-1002	Sequence 1002, Ap
24	167	5.7	1113	7 US-11-055-822-368	Sequence 368, App
25	167	5.7	1113	7 US-11-055-822-1000	Sequence 1000, Ap

26	110	3.8	408	7 US-11-055-822-910	Sequence 910, App
27	101.5	3.5	371	6 US-10-793-626-3294	Sequence 3294, Ap
28	98.5	3.4	947	6 US-10-453-372-1010	Sequence 1010, Ap
29	98.5	3.4	1579	7 US-11-052-554A-9	Sequence 9, Appl
30	97.5	3.4	3073	7 US-11-143-980-50	Sequence 50, Appl
31	96.5	3.3	230	6 US-10-793-626-3314	Sequence 3314, Ap
32	96.5	3.3	717	6 US-10-467-657-8056	Sequence 8056, Ap
33	96	3.3	393	6 US-10-485-517-316	Sequence 316, App
34	96	3.3	512	6 US-10-519-531-4	Sequence 4, Appl
35	96	3.3	512	6 US-10-519-531-5	Sequence 5, Appl
36	96	3.3	610	7 US-11-055-822-1146	Sequence 1146, Ap
37	96	3.3	610	7 US-11-124-291-6	Sequence 6, Appl
38	95.5	3.3	544	7 US-11-166-609-18	Sequence 18, Appl
39	95.5	3.3	1417	7 US-11-052-554A-8	Sequence 8, Appl
40	95	3.3	423	7 US-11-070-080-16	Sequence 16, Appl
41	95	3.3	3507	7 US-11-075-185-7	Sequence 7, Appl
42	94.5	3.3	583	7 US-11-080-991-64	Sequence 64, Appl
43	94.5	3.3	2233	6 US-10-873-528-2	Sequence 2, Appl
44	94	3.2	386	6 US-10-497-135-20	Sequence 20, Appl
45	94	3.2	769	6 US-10-467-657-3280	Sequence 3280, Ap

ALIGNMENTS

RESULT 1  
US-11-186-999-14  
; Sequence 14, Application US/11186999  
; Publication No. US20060019364A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS  
; FILE REFERENCE: BMS Docket Number 10245 NP  
; CURRENT APPLICATION NUMBER: US/11/186,999  
; CURRENT FILING DATE: 2005-07-21  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 2455  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-11-186-999-14

Query Match 61.1%; Score 1777.5; DB 7; Length 2455;  
Best Local Similarity 63.4%; Pred. No. 2.5e-131;  
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;

QY	22	ASPVADPIRKQGGHVSITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED	81
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QY	82	LKNADYIRMDADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES	141
DB	301	LKANAERYIKMDADQYVPVPGPGNNNNYANVELIIDIARIKIPVQAVWAGWGHASENPKLPEL	360
QY	142	LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPVCMPSWGSGTGKETMMSD---	197
DB	361	LC--KHEIAFLGPPSEAMWALGDKISSTIVAQTLPWSSGSLTVEWTEDSQHQKC	418
QY	198	LTVSDVYQACIHTAEGLEKAEKIGYPMVMIKASEGGGKGIRKCTNGEEFKQLYNVL	257
DB	419	ISVPEDVYEQGCVRDVDEGLQAAEKVGFFPLMIKASEGGGKGIRRAESAEDFPMLEFRQVQ	478
QY	258	GEVPGSPFVVMKLAGQARHLEVQLLADQYGNIAISIFGRDCSVQRRHQKIIIEAPVTIAPE	317
DB	479	SEIFGSPFIFLMKLAQNARHLEVQVLADQYGNVSLFGRDCSVQRRHQKIIIEAPATIAAP	538
QY	318	DARESMKAAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLNRLQVEHPHPTTEMVSGVNI	377
DB	539	AVTEFMEQCAVLLAKTGVYSAGTVEYLYS-QDGSFHFLNRLQVEHPHPTTEMVSGVNI	597
QY	378	PAQLQVAMGIPLYSIDRTLYGMDPRGNEVIDFDSSPSFKTQKPKQ-PQGHVVACR	436

Db 598 PAAQLQIANGVPLHRLKDIRLLYGESPWG-----VTPVSFETPLSPPIARGHVIAAR 649  
QY 437 ITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE 496  
Db 650 ITSENPDGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSGWGENREE 709  
QY 497 ARKOMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGDGLIQDRLTAERPPAD 556  
Db 710 AISNMVVALKELSIRGDFRTTVEYLVNLTETESFQNNIDTGWLDHLIAQRVQAEKPDIM 769  
QY 557 LAV 559  
Db 770 LGV 772

RESULT 2  
US-11-186-999-16  
; Sequence 16, Application US/11186999  
; Publication No. US20060019364A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS  
; FILE REFERENCE: BMS Docket Number 10245 NP  
; CURRENT APPLICATION NUMBER: US/11/186,999  
; CURRENT FILING DATE: 2005-07-21  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 2455  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-11-186-999-16

Query Match 61.1%; Score 1777.5; DB 7; Length 2455;  
Best Local Similarity 63.4%; Pred. No. 2.5e-131;  
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;  
QY 22 ASPVADFIRKQGHSHSVITKVLICNNGIAAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
Db 242 ASP-AEFVTRFGGNRVETVLIANNNGIAAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPED 300  
QY 82 LKVNADYIRMADQYVEVPVPGGNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141  
Db 301 LKANAIEYIKMADQYVPVPGGNNNNYANVELIIDIAKRIPQAVWAGWGHASENPKLP 360  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---QG-F 197  
Db 361 LC--KHEIAFLGPPSEAMWALGDKISSTIVAQTLPWSSGLTVEWTEDSQHGKC 418  
QY 198 LTVSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVL 257  
Db 419 ISVPEDVYEQGCVRDVDEGLQAAEKVGFPLMIKASEGGGKGIRRAESAEDFPMLFRQVQ 478  
QY 258 GEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVTIAPE 317  
Db 479 SEIPGSPIFLMKLAQNARHLEVQVLADQYGNVSLFGRDCSIQRRHQKIIIEAPATIAAP 538  
QY 318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPPTTEMVSGVNI 377  
Db 539 AVPEFMEQCAVLLAKTVGYVSAGTVEYLYS-QDGSFHFLNPRLQVEHPCTEMIADVNL 597  
QY 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTKRPQ-PQGHVVACR 436  
Db 598 PAAQLQIANGVPLHRLKDIRLLYGESPWG-----VTPVSFETPLSPPIARGHVIAAR 649  
QY 437 ITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE 496  
Db 650 ITSENPDGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSGWGENREE 709  
QY 497 ARKOMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGDGLIQDRLTAERPPAD 556  
Db 710 AISNMVVALKELSIRGDFRTTVEYLVNLTETESFQNNIDTGWLDHLIAQRVQAEKPDIM 769

QY 557 LAV 559  
Db 770 LGV 772  
RESULT 3  
US-11-144-368-4  
; Sequence 4, Application US/11144368  
; Publication No. US20050272082A1  
; GENERAL INFORMATION:  
; APPLICANT: Kan, Zhengyan  
; APPLICANT: Garrett-Englele, Philip W.  
; APPLICANT: Armour, Christopher D.  
; APPLICANT: Raymond, Christopher K.  
; APPLICANT: Castle, John C.  
; TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORM OF  
; TITLE OF INVENTION: ACETYL-COA CARBOXYLASE 2 (ACC2)  
; FILE REFERENCE: RS0220  
; CURRENT APPLICATION NUMBER: US/11/144,368  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: 60/577,234  
; PRIOR FILING DATE: 2004-06-04  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 2256  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-368-4

Query Match 60.9%; Score 1769.5; DB 7; Length 2256;  
Best Local Similarity 63.4%; Pred. No. 9.6e-131;  
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;  
QY 22 ASPVADFIRKQGHSHSVITKVLICNNGIAAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
Db 43 ASP-AEFVTRFGGDRVIEKVLIANNGIAAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPED 101  
QY 82 LKVNADYIRMADQYVEVPVPGGNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141  
Db 102 LKANAIEYIKMADHYVPVPGGNNNNYANVELIIVDIKRIPQAVWAGWGHASENPKLP 161  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---QG-F 197  
Db 162 LC--KNGVAFGLGPPSEAMWALGDKIASTVVAQTLOVPTLPWSSGSLTVEWTEDDLOQGKR 219  
QY 198 LTVSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVL 257  
Db 220 ISVPEDVYDKGCVKVDDEGLEAAERIGFPLMIKASEGGGKGIRKAESAEDFPILFRQVQ 279  
QY 258 GEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVTIAPE 317  
Db 280 SEIPGSPIFLMKLAQHARHLEVQILADQYGNVSLFGRDCSIQRRHQKIVEEAPATIAPL 339  
QY 318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPPTTEMVSGVNI 377  
Db 340 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLNPRLQVEHPCTEMIADVNL 398  
QY 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKT-QRKPPQGHVVACR 436  
Db 399 PAAQLQIANGVPLHRLKDIRLLYGESPWG-----VTPISFETPSNPPLARGHVIAAR 450  
QY 437 ITAENPDTGFKPGMGALTTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE 496  
Db 451 ITSENPDGFKPSSGTVQELNFRSNKNVWGYFSVAAATGGLHEFADSQFGHCFSGWGENREE 510  
QY 497 ARKOMVISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLGDGLIQDRLTAERPPAD 556  
Db 511 AISNMVVALKELSIRGDFRTTVEYLVNLTETESFQNNIDTGWLDYLIAEKVQAEKPDIM 570  
QY 557 LAV 559  
Db 571 LGV 573













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; APPLICANT: Andaxmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1317
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1317

Query Match      22.0%; Score 640.5; DB 6; Length 703;
Best Local Similarity 31.8%; Pred. No. 1.1e-42;
Matches 166; Conservative 87; Mismatches 178; Indels 91; Gaps 12;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVP 99
Db 40 KILVANRGEIACRVIRTKMGIKT-----VAIHSVDVASSVHVWMADEAVCVG 88

QY 100 GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 89 PAPTCKSYLNMDAIMEAIKKTQRAQVHPGYGFLSENEKFARCLAA--EDVVFIGPDTHAI 146

QY 160 RSLGDKISSTIVAQAHDVPCMPWSGTGIRKCTNGEFGKQLYNVAVLGEVPS-----PVFVWKLQAGAR 275
Db 147 QAMGDKIESKLLAKKAEVNTIP-----GFDGVVKD-----ABEAVRI 183

QY 220 AEKIGYPVMIKASEGGGKGIRKCTNGEFGKQLYNVAVLGEVPS-----PVFVWKLQAGAR 275
Db 184 AREIGYPVMIKASAGGGGKGMRIAWDDETRDGFRLSSQEAASSFGDDRLLEKFIIDNPR 243

QY 276 HLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVG 335
Db 244 HIEIQVLGDKHGNALWLNRECSIQRRNQKVVBEAPSFILDAETRRAMGEQAVALARVK 303

QY 336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPHTTEMVSGVNIIPAAQLQVAMGIPLYSIR 394
Db 304 YSSAGTVEFLVDSKK-NFYFLEMNTRLQVEHPHTTECITGLDLVQEMIRVAKGYPLRHQA 362

QY 395 DIRTYGMDPRGNEVIDDFSSPESFQTKRQKQPGQHVHVACRITAENPDGTF-KPGMGAL 453
Db 363 DIRI-----NGWAVECRVYAEDEPYKSFGLPSIGRL 392

QY 454 TE-----LNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVIS 504
Db 393 SQYQEPHLPGVRVDSGIQPGSDISI-----YYDPMISKLITYGSDRTEALKRMADA 444

QY 505 LKELSIRGDFRTTVEYLKLETDAPESNKITTGWLDGLIQD 546
Db 445 LDNYVIRG-VTHNIALLEVIINSRFRVKGDIKSTKFLSDVYPD 485

RESULT 14
US-10-793-626-2448
; Sequence 2448, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2448
; LENGTH: 1151

```

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2448

```

Query Match 21.5%; Score 625; DB 6; Length 1151;  
Best Local Similarity 31.8%; Pred. No. 3.7e-41;  
Matches 164; Conservative 91; Mismatches 182; Indels 78; Gaps 14;

```

QY 38 ITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYVE 97
Db 8 IKKLLVANRGEIAIRIFRA-----AAELNISTVAIYSNED-KSSLHRYKADESYLV 57

QY 98 VPGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGS 157
Db 58 GSDLGPAESYLNIERIEVALRAGVDIAHPGYGFLSENEQFARRCA--EEGIKFIGPHLE 115

QY 158 AMRSLGDKISSTIVAQAHDVPCMPWSGTGIRKCTNGEFGKQLYNVAVLGEVPS-----GSPVFMKLAGQ 273
Db 116 HLDPMFGDKVKARTAINANLPVIP--GT-----DGFIESFEAAE 152

QY 218 EAKKIGYPVMIKASEGGGKGIRKCTNGEFGKQLYNVAVLGEVPS-----GSPVFMKLAGQ 273
Db 153 QFANEAGYPLMIKATSGGGGKGMRIVRRESSELEDAFHRAKSEAEKSGFNSEVYIERIDN 212

QY 274 ARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKL 333
Db 213 PKHIEVQVIGDEFNGNIHLIERDCSVQRRHQKVVVEAPSVGLSNKLRERICDAAIQLMEN 272

QY 334 VGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPHTTEMVSGVNIIPAAQLQVAMGIPLYSI 393
Db 273 IKYVNAGTVEFLVSGD--EFFFIEVNPVRVQVEHTTIMITGIDIVKTQILVADGESLF-- 328

QY 394 RDIRTYGMDPRGNEVIDDFSSPESFQTKRQKQPGQHVHVACRITAENPDGTFKPGMGAL 453
Db 329 -----GDKI-----SMPQQNEIQTLGYAIQCRITTEDPTNDFMPDSG-- 365

QY 454 TELNFRSSTSTWGYFSV-----GTSGA-LHEYADSQFGHIFAYGADRSEARKQMVISLK 506
Db 366 TIIAYRSS-----GGFGVRLDAGDGFQGAIEISPYDSSLVLLKSLTHAVSFQAEKMERSLR 421

QY 507 ELSIRGDFRTTVEYLKLETDAPESNKITTGWLD 541
Db 422 EMIRIG-VKTNIPFLINVMRNDKFRSGDYTTKFI 455

```

RESULT 15  
US-10-858-730-12  
; Sequence 12, Application US/10858730  
; Publication No. US20050255568A1  
; GENERAL INFORMATION:  
; APPLICANT: Bailey, Richard B.  
; APPLICANT: Blomquist, Paul  
; APPLICANT: Doten, Reed  
; APPLICANT: Driggers, Edward M.  
; APPLICANT: Madden, Kevin T.  
; APPLICANT: O'Leary, Jessica  
; APPLICANT: O'Toole, George  
; APPLICANT: Trueheart, Joshua  
; APPLICANT: Walbridge, Michael J.  
; APPLICANT: Yorgey, Peter S.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID  
; FILE REFERENCE: 14184-030001  
; CURRENT APPLICATION NUMBER: US/10/858,730  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/475,000  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: US 60/551,860  
; PRIOR FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 364



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-208

Query Match      18.7%; Score 543.5; DB 6; Length 1140;
Best Local Similarity 29.3%; Pred. No. 9.5e-35;
Matches 157; Conservative 90; Mismatches 188; Indels 101; Gaps 16;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLVKNADYIRMADQYVEV- 98
Db 14 KILVANRGEIAVRAFR-----ALETGA-----ATVAIYPREDR-GSFHRSFASEAVRIG 62

QY 99 PGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSA 158
Db 63 TEGSPVKAYLDIDEIIGAAGKKVADAIYPGYGFLSENAQLARECA--ENGITFIGPTPEV 120

QY 159 MRSLGDKISSITIVAQHADVPKMPWSGTGKIKETMMSDQGLTVSDVVYQQACIHTAEGL 218
Db 121 LDLTGDKSRAVTAAGKAGLPVLAES-----TPSKNI-----DEIVK 156

QY 219 KAEKIGYPMIKASEGGGKGIKCTNGEEFKQLYNALVGEVPGS-----PVFVVKLAGQA 274
Db 157 SAEQOTYPIFVKAVAGGGGRGFRFVSPDELRLKATEASRAEAAFGDGAVYVERAVINP 216

QY 275 RHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLV 334
Db 217 QHIEVQILGDHTGEVHLYERDCSLQRRHQKVEIAPQAHLDPELRDRICADAVKCRSI 276

QY 335 GYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIR 394
Db 277 GYQAGTVEFLVD-EKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMLAAGATLKEL- 334

QY 395 DIRTYGMDPRGNEVIDDFESSPESFQKQKPOQGHVACRITAENPDGFKPGMGALT 454
Db 335 -----GL-----TQDKIKTHGAALQCRITTEDPNNGFRPDGTGIT 369

QY 455 ELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY-----GADRSEARKQMVI 503
Db 370 -----AYRSPGGAGVRLDGAALQGEITAHFDSMLVKWTCRGSDFETAVARAQR 418

QY 504 SLKELSIRGDFRTTVEYLKLETDAFESNKITTGWL---DGLIQDRLTAERPPAD 556
Db 419 ALAEFTVSG-VATNIGFLRALLREEDFTSKRIATGFIADHPHLLQ-----APPAD 467

RESULT 18
US-10-793-626-218
; Sequence 218, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 218
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-218

Query Match      17.6%; Score 512.5; DB 6; Length 341;
Best Local Similarity 31.7%; Pred. No. 4.5e-33;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETF-----GDERAIEFTVMATPEDLVKNADYIRMADQ 94
Db 4 RCLIANRGEIAVRIIRACRELNIETVAIYAKGDE-----NSLHVSLADQ 47

QY 95 YVEVPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGP 154
Db 48 AICIGBANPLDSYLNIDRIISAQKVTESNVHPGYGFLSESTNFAK--AVEDNHIHFIGP 105

QY 155 PGSAMRSLGDKISSITIVAQHADVPKMPWSGTGKIKETMMSDQGLTVSDVVYQQACIHTAE 214
Db 106 SKTTMEMMGDKITARQTVKQAGVPVPGSNDVAQ-----SVD 142

QY 215 EGLEKAEKIGYPMIKASEGGGKGIKCTNGEEFKQLYNALVGE-----VPGSPVFMKL 270
Db 143 EIKLLSKEIGFPVVLKAASGGGGKGIKIVKEASHLDQALKEAKSEGGQKYNDDRIVVEAF 202
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Matches 121; Conservative 61; Mismatches 121; Indels 79; Gaps 7;

QY 175 ADVPCMPWSGTGKIKETMMSDQGLTVSDVVYQQACIHTAEGLKAEKIGYPMIKASEG 234
Db 14 ANVPVVPGS-----EGLIQSIDDAKKIAGKIGYPVVIKATAG 50

QY 235 GGGKGIKCTNGEEFKQLYNALVGEVP-----GSPVFVVKLAGQARHLEVQLLADQYGNAI 290
Db 51 GGCKGIRVARDEKELETGYRMTQQAETAFAFGNGGLYLEKPIENFRHIEIQIIGDTYGNVI 110

QY 291 SIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES 350
Db 111 HLGERTCTIQRMQKLVVEAPSPVLSEDKRQEMGNAAIRAAKAVNYENAGTIEFIYDLDD 170

QY 351 GEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVI 410
Db 171 NQFYFEMEMNTRIQVEHPVTETMTGVDLVKLQKVAMG-----EAL 210

QY 411 DFDSSPESFQKQKPOQGHVACRITAENPDGFKPGMGALTTELNFRSSTSTWGYFSV 470
Db 211 PF-----KQEDISINGHAIEFRINAENPYKNFMPSPGKITQ-----YLAP 250

QY 471 G-----TSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVE 519
Db 251 GGFGVRIESACTYNTIPPYDSMVAKLIVHEPTREESIMTGIRALSEYLVG-IDTTIP 309

QY 520 YLIKLETDAFESNKITTGWLD 541
Db 310 FHLRLNNHIFRSGEFTNKFLE 331

RESULT 19
US-10-793-626-804
; Sequence 804, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 804
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-804

Query Match      17.5%; Score 508.5; DB 6; Length 453;
Best Local Similarity 27.7%; Pred. No. 1.4e-32;
Matches 144; Conservative 95; Mismatches 184; Indels 97; Gaps 12;

QY 40 KVLICNNGIAAVKEIRSIRKWAYETF-----GDERAIEFTVMATPEDLVKNADYIRMADQ 94
Db 4 RCLIANRGEIAVRIIRACRELNIETVAIYAKGDE-----NSLHVSLADQ 47

QY 95 YVEVPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGP 154
Db 48 AICIGBANPLDSYLNIDRIISAQKVTESNVHPGYGFLSESTNFAK--AVEDNHIHFIGP 105

QY 155 PGSAMRSLGDKISSITIVAQHADVPKMPWSGTGKIKETMMSDQGLTVSDVVYQQACIHTAE 214
Db 106 SKTTMEMMGDKITARQTVKQAGVPVPGSNDVAQ-----SVD 142

QY 215 EGLEKAEKIGYPMIKASEGGGKGIKCTNGEEFKQLYNALVGE-----VPGSPVFMKL 270
Db 143 EIKLLSKEIGFPVVLKAASGGGGKGIKIVKEASHLDQALKEAKSEGGQKYNDDRIVVEAF 202
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Qy 271 AGQARHLEVLQADQYGNASIFGRDCSVORRHQKIIIEAPVTIAPEDARESMEKAAVRL 330  
Db 203 IPVAKHVEVQIIGDGKNNVHLGERDCSVORRKNQKLIIEAPCAALTEERTRICGDAVKV 262  
Qy 331 AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPL 390  
Db 263 AQASRYRSAGTIEFLVTEDA--HYFIEMNARIQVEHTVTEMRADRDLLQAQLYL----- 314  
Qy 391 YSIRDITLYGMDPRGNEVIDDFSSPESFKTQKPKPOQGHVAVACRITAENPDGFKPGM 450  
Db 315 -----LTHGELPFTQKDILFN-----GHVIEARINAENPEKNFLPTP 351  
Qy 451 GALTENFRSSTSTWGYFSVGTSGALH-----EYADSQFGHIFAYGADRSEARKQMVIS 504  
Db 352 GKVNKLHLPOG-----FNIRVDSLLTYGQVSPYDLSLVAKVIKDSNRQTAINKLKVA 405  
Qy 505 LKELSIRGDFRTTVEYLKLETDFAF---ESNKITTGWLD 541  
Db 406 LDEMVIIEG-FTTADFLYAVLNYPYIAKGDASKVDIKFLE 444

RESULT 20  
US-10-793-626-648  
; Sequence 648, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 648  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (309)  
; OTHER INFORMATION: variable amino acid  
US-10-793-626-648

Query Match 16.8%; Score 487; DB 6; Length 309;  
Best Local Similarity 31.8%; Pred. No. 3.9e-31;  
Matches 117; Conservative 53; Mismatches 108; Indels 90; Gaps 7;  
Qy 175 ADVPCMPWSGTGIKETMMSDQGLTVSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEG 234  
Db 14 ANVPVPGS-----EGLIQSIDDAKKIARKIGYPVIAKATAG 50  
Qy 235 GGGKGIRKCTNGEEFKQLYNVAVLGEVP---GSPVFMKLAGQARHLEVQLLADQYGNAI 290  
Db 51 GGGKGIRVARDEKELETGYRMTQQAETAFGNGGLYLEKFIENFRHIEIIGDTYGNVI 110  
Qy 291 SIFGRDCSVORRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES 350  
Db 111 HLGERDCTIQRMQKLVVEAPSPVLSEDKRQEMGNAAIRAAKAVNYENAGTIEFIYDLDD 170  
Qy 351 GEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVI 410  
Db 171 NQFYFEMNTRIQVEHPVTEMTGVDLVKLQKVAMG-----EAL 210  
Qy 411 DFDSSPESFKTQKPKQGHVAVACRITAENPDGFKPGMGALTELNFRSSTSTWGYFSV 470  
Db 211 PF-----KQEDISINGHAIEFRINAENPYKNFMPSPGKITQ-----YLAP 250

Qy 471 G-----TSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTIVE 519  
Db 251 GGFGVRIESACYTNYTIPPPYDSMVAKLIVHEPTREE-----SMTGIRALSE 298  
Qy 520 YLIKLELET 527  
Db 299 YLVLGIDT 306  
RESULT 21  
US-10-467-657-1654  
; Sequence 1654, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 1654  
; LENGTH: 1071  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1654

Query Match 6.1%; Score 178; DB 6; Length 1071;  
Best Local Similarity 21.8%; Pred. No. 4.9e-06;  
Matches 79; Conservative 66; Mismatches 162; Indels 56; Gaps 15;  
Qy 211 HTAEEGLEKAEKIGYPVMIKAS--EGGGKGIRKCTNGEEFKQLYNVAVLGEVPGSPVFM 268  
Db 150 HTMNEALAAQEQVGFTLIRPSFTMGSGGGI--AYNKDEFLAICERGFDASPTHELLIE 207  
Qy 269 KLAGQARHLEVQLLADQYGNASISIFGRDCSVORRHQKIIIEA-PVTIAP-----EDARES 322  
Db 208 QSVLGWKEYEMEVRDKADNCIII---CSIENFDPMGVHTGDSITVAPAQTITDKEYQI 263  
Qy 323 MEKAAVRLAKLVGYVSAGT-VEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQ 381  
Db 264 MRNASLAVLREIGVDTGGSNNQFAVNPENGEMIVIEVMPVSRSSALASKATGFPIAKVA 323  
Qy 382 LQVAMGIPLYSIR-DI---RTLYGMDPRGNEVIDDFSSPESFKTQKPKQGHVAVACRI 437  
Db 324 AKLAVGFTLDELNDITGRTTPASPEPS----IDYVVTKIPRFAFEKFPAAADD-----RL 374  
Qy 438 TAENPDGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA 497  
Db 375 TTQMKSVGEVMMAMGRTIQESFQKALRG---LETGLCG-----FNPRSEDKAEI 419  
Qy 498 RKQMVISLKE--LSIRGDFRT--TVEYLIKLETDAFESNKITTGWLDGLIQDRLTAERP 553  
Db 420 RRELANPGPERMLFVADAFRAGFTPEEIEICAIDP-----WFLAQIEDLMKEEKS 470  
Qy 554 PAD 556  
Db 471 VSD 473

RESULT 22  
US-11-055-822-370  
; Sequence 370, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard







QY	497	IFAYGADREARKQWISLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWL	540
Dd	976	VFTVVARND--KRTLLPIQRLALMG-----YKILATEG-----TAGWL	1012

```

RESULT 26
US-11-055-822-910
; Sequence 910, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper on
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 910
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-910.

```

	Query Match	3.8%;	Score 110;	DB 7;	Length 408;
	Best Local Similarity	21.6%;	Pred. No. 0.27;		
	Matches	90;	Conservative	66;	Mismatches 172; Indels 88; Gaps 21;
QY	39	TKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNVADYIRMADQYVEV	98		
Db	16	TKVMLLGS-----ELGKEVAIAFORLG-----LEVHA-----VDRYEHA	50		
QY	99	PGGSNNNYANVDLIVDAERAGVHAVWAGWGHASENPR-----LPESLAASKHIIFGP	154		
Db	51	PA-----HQVAHFSYVIDMTDAAQVREL-----VERVPDFVIPEIEALATDELVKIEE	99		
QY	155	PGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGLTVSDDVYQQACIHTAE	214		
Db	100	EGLA-----TIVPT-ARAAKLTMNREGIRKLAABELGLPTSN-----YEFC-STFE	143		
QY	215	EGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALV--GEVPGSPFV---MK	269		
Db	144	EFSAAAEKLGYPNVVKPVMSSSGKQSVLRSSDDLQAADWYAMSGARVANSRVIVEAFVE	203		
QY	270	LAGQARHLEVQLLADQYGNIAISIFGRDCSVQRRHQKIEE-APVTIAPEDARESMEKAAV	328		
Db	204	FDYEITLLTVRSIDPTTSKPATWFCEPIGHRQEDGDYVESWQPMEMTPR-ALENARSVA	262		
QY	329	RLAKLVGYVSAGTVENLYSPESGEFAFLELNPRLQVEHPT-----TEMVSGVNIPA-AQ	381		

Db	263	RITNALGGRGVFGVELFVSGD--DVYFSEVSPR---PHDTGLVTLATQRFSEFELHAKAI	317
QY	382	LQVAMGIPLYISIRDITLY-GMDPRGNE-----VIDFD---FSSPESFKTQR	424
Dd	318	LGLPVDVTLISPGASAVYGGIESEGVSYTGLAEALAVAETDLRIFAKPEAFTKRR	373

RESULT 27  
US-10-793-626-3294  
; Sequence 3294, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3294  
; LENGTH: 371  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-3294

Query Match	3.5%	Score 101.5;	DB 6;	Length 371;
Best Local Similarity	24.6%;	Pred. No. 1.1;		
Matches 34;	Conservative 21;	Mismatches 62;	Indels 21;	Gaps 3
QY	149	IIFIGPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVDVVYQQA	208	
Db	119	IPYVGVNGVLAASSSMDKLVMKQLFHEHRLPQLPYI-----SFLRSEYEKEYENN	166	
QY	209	CIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGCEEFKQLYNVAVLGEVPGSPVFVM	268	
Db	167	IIKLVN-----DKLTPYFVKVPANLGSSVGISKCNNEELK---SGIAEAFQFDRKLVI	217	
QY	269	KLAGQARHLEVQLLADQY	286	
Db	218	EQGINAREIEVAVLGNDY	235	

RESULT 28  
US-10-453-372-1010  
; Sequence 1010, Application US/10453372  
; Publication No. US20060003323A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook, et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-589 A  
; CURRENT APPLICATION NUMBER: US/10/453,372  
; CURRENT FILING DATE: 2003-06-03  
; PRIOR APPLICATION NUMBER: 09/789390  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/185967  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 09/823187  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195792  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 09/839446  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 60/199476  
; PRIOR FILING DATE: 2000-03-25  
; PRIOR APPLICATION NUMBER: 09/863776  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/208263

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; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1010
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1010

Query Match      3.4%; Score 98.5; DB 6; Length 947;
Best Local Similarity 19.1%; Pred. No. 7.3;
Matches 94; Conservative 70; Mismatches 144; Indels 183; Gaps 27;

QY 124 AVWAGWGHASENPRLL-----PESLAASKHK-----IIFIGP---PGSAMR-----S 161
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 ALGVSWCPATWHPRLDMGRHLRPRSTSYRNLPHLFLFVGFVGFSLGSGYSRATLLEYS 67

QY 162 LGDKISSIV--AQHADVPCMPWSG-----TGIK-----ETMSDQG-----FL 198
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 LNEGLPAGVLIGSLAEDRLRLPRSGRPDPQSQLPERTGAENWNPPLSFLASRGLSGQYV 127

QY 199 TVSDDVYQACIHTAEGLEKAEKIGYPMIKASEGGGKGIRKCTNGEEFKOLYNAVLG 258
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 TLDN---RSGELHTSAQEIDRE-----ALCVEGGGG-----TAWSG 160

QY 259 EV-----PGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEAPVT 313
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 SVSISSPSDSCLLL-----LDVLVLPOEYFRFVK-----VK 192

QY 314 IAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVS 373
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 IAIRDINDNAPQFPVSQISV-----WV--PENA-----PVNTRLAIEHPAVIDPV 235

QY 374 GVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFESSPESEFQTKRP----- 426
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 GIN-----GVQTYRLLDYHGMFTLDVEENE-----NGERTPYLLIWMGA 273

QY 427 ---QPQGHVVACRITAENPDTGFKPGMGALT-----ELN-----FRSS---TSTWGYFS 469
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 274 LDRETQDYVSI-ITAE--DGGSPPLLGSAATLTIGISDINDNCPLFTDSQINVTYGNAT 330

QY 470 VGTSGALHEYADSQFGH----IFAYGADRSEARKQMVISLKELSIKELSGDFRTTVEYLKLL 525
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 VGTPIAAVQAVDKDLGTNAQITYSYSQVPQASKOL-----FHLDENTGVIKLFSKI 382

QY 526 ETDAFESNKIT 536
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 GGSVLESHKLT 393

RESULT 29
US-11-052-554A-9
; Sequence 9, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
```

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; LENGTH: 1579
; TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-9

Query Match      3.4%; Score 98.5; DB 7; Length 1579;
Best Local Similarity 19.6%; Pred. No. 15;
Matches 125; Conservative 68; Mismatches 198; Indels 247; Gaps 27;

QY 4 DHKAVSQFIGGNPLETAPSPVADFIRKQGGHSHVIT-----KVLJ---CNNGIAAVKE 53
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 965 DNKTFS-----LSVLPDESSAKVISITGAEKITVGENITLRLVQDAFNNTVIAGQRV 1017

QY 54 IRSIRKWAYETFGDERAIEFTVMATPEDLVNADYIRMADQYVEVPGSGNNNNNYANVDLI 113
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1018 RLQAQPTTNITIGD-----TAYTDNNGYAVVNL 1046

QY 114 VDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSITVAQ 173
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1047 ---STQPGVYQVTTATLDNNSSS-KVDVNVANGKLELTSSKPETTVHNSEG---ITLTATAR 1100

QY 174 HADVPCMP-----WSGTGIKETMMSDQGFLLTVSDD---VYQACI----- 210
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1101 NARGELMPGQIITFSVTPEGATLSNTGEVLTDQSGQAKVTLTSDKVNVTVTATMGKDVP 1160

QY 211 -----HTAE-----EGLEKA-----EKIGYPVM-IKASEGGG 236
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1161 VQSQVTVAVKADAKTAHVSVSWASPDITADGDSSTITSRVEDDYGFPVEGDISHGLD 1220

QY 237 GKG-----IRKCTNGEEFKQLYN-----AVLGEVPG----- 262
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1221 TKGSPVNVNIPTRTDQSGQVTTATITSTLAETLVNVQVPGTANQASATITLVAGTADSKS 1280

QY 263 ---SPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPEDA 319
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1281 ILKSDVDTLKADYQQSAKLTLTLDQKYGNI-----VTSDFLEFVQSGPF----- 1325

QY 320 RESMEKAAVRLAKL--VGIVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1326 -----VNFLKLSDDIDYSQRNYGEYTVTVTGCKEGTATLIP-----MLNGVH- 1366

QY 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFESSPESEFQTKRPQPGHVVACR- 436
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1367 -----QANLSISLNLISQIKEM-----SGHVTANNH 1392

QY 437 ---ITAENPDTGFKPGMGALTTELNFRSS-----TSTWGYFSVGTSGALHEYADSQFGH 486
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1393 TFASTKFPSEGFAGAYYTLNNDNFAGKTVDYMFSSSQGWVSVDASGKVS----- 1443

QY 487 IFAYGADRSEARKQMVISLKELSIKELSGDFRTTVEYLKLL 524
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1444 -FANIGD-----QTSVTISAVPROGG--TTYQTLIKL 1472
```

```
RESULT 30
US-11-143-980-50
; Sequence 50, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Haltli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; TITLE OF INVENTION: Polyketide
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
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RESULT 29
US-11-052-554A-9
; Sequence 9, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
```







Db 275 RMYSPSILDIRQPKPEPRDYDRFYKTLRAEQASQEVKNW----MTETLLVQNPDC 330  
QY 201 SDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNALVGEV 260  
Db 331 KTIKALGPAATLEE-----MMTACQGVGGPGCHKARVLAEAMSVQTSAT--- 375  
QY 261 PGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRR-----HQKIIEEA 310  
Db 376 -----IMQNGNFRNQRKIVKFCNGKEGHI-ARNCRAPRKGCWKCKEGHQ----- 422  
QY 311 PVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYS-PESGEFAFLELNPRLOVEHPTT 369  
Db 423 -----MKDCTERQANFLGKIWPSYKGRPGNFGLOSRRPEPTAPPFLOSRPE-PTAPPEE 473  
QY 370 EMVSGVNIPA-AQLQVAMGIPLYSIDRTLYGMNDP 404  
Db 474 SFRSGVETTPSQKQEPIDKELYPLTSLRSLFGNDP 509

RESULT 36  
US-11-055-822-1146  
; Sequence 1146, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; FILE REFERENCE: BGI-121CPCN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 1146  
; LENGTH: 610  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum

US-11-055-822-1146  
Query Match 3.3%; Score 96; DB 7; Length 610;  
Best Local Similarity 20.9%; Pred. No. 6;  
Matches 102; Conservative 59; Mismatches 188; Indels 140; Gaps 22;  
QY 64 TFGDERAIEFTVMATP--EDLKNVADYIRMADQYVEVPGGSNNNNY----- 107  
Db 145 TFSDEGTGFEVVDKLPYLRDLGVTAIELLPVQPF-----GGNRNWGYDGVLWHAVHAGYGG 200  
QY 108 -ANVDLIVDVAERAGVHAVW-----AGW-----GHAS 133  
Db 201 PAGLKKLIDASHQAGI-AVYLDVVYNHFGPDGNYNGQFGPYTSGSGTGWGDVVNINGHDS 259

QY 134 ENPRLPESLAASKHKIIFIGPPG---SAMRSLGDKISSTIVAQAHDVPCMPWSGTG--- 186  
Db 260 DEVR-NYILDAARQWFEDFHVVDGLRLDAVHSLDDRGAYSLLAQLTWAEDVSAQTGIPRS 318  
QY 187 -IKETMMSDQGFLLTVSD-----DVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKG 239  
Db 319 LIAESELNDPKFVTSREAGGGLDAQWVDDIHHALHALVSGERNY-----YSDFGSVDT 373  
QY 240 IRKCTNGEEFKQL--YNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDC 297  
Db 374 LAK-TLREVEFHTGNYSTYGRNHNHGRPVH-PDITPASRFVYTYTTHDQTGNR-AIGDRPS 430  
QY 298 SVQRRHQKIIIEEAPVTIAP-----EDA 319  
Db 431 TTLTPEQQVLKAAIIYSSPYTPMLFMGEEFGATTFFAFPCSHTDPELNRLTSEGRKREFA 490  
QY 320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEF-----AFLELNPRLOVEHP---TTEM 371  
Db 491 RLGWNADDIPSPELESTFTSSKLDWEFTAQRINDAYKQLLHLRHLTLGFSQPNLLTLEV 550  
QY 372 VSGVNIPAAQLQVAMG---IPLYSIDRTLYGMDPRGNEVIDFDFSSPESFKTQKPKQ 427  
Db 551 EHEN---WLSMANGRILANFSDDTITV-----PLGELI-YSFTSPTVTDSTTLQ 600  
QY 428 PQGHVVACR 436  
Db 601 PWGFAILTR 609  
RESULT 37  
US-11-124-291-6  
; Sequence 6, Application US/11124291  
; Publication No. US20050266536A1  
; GENERAL INFORMATION:  
; APPLICANT: WOLF, ANDREAS  
; APPLICANT: SCHISCHKA, NATALIE  
; APPLICANT: HERMANN, THOMAS  
; APPLICANT: MORBACH, SUSANNE  
; APPLICANT: KRAEMER, REINHARD  
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-AMINO ACIDS USING  
; FILE REFERENCE: 223168US0X  
; CURRENT APPLICATION NUMBER: US/11/124,291  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US/10/212,219  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US 60/316,276  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: DE 101 39 062.9  
; PRIOR FILING DATE: 2001-09-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 610  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-124-291-6  
Query Match 3.3%; Score 96; DB 7; Length 610;  
Best Local Similarity 20.9%; Pred. No. 6;  
Matches 102; Conservative 59; Mismatches 188; Indels 140; Gaps 22;  
QY 64 TFGDERAIEFTVMATP--EDLKNVADYIRMADQYVEVPGGSNNNNY----- 107  
Db 145 TFSDEGTGFEVVDKLPYLRDLGVTAIELLPVQPF-----GGNRNWGYDGVLWHAVHAGYGG 200  
QY 108 -ANVDLIVDVAERAGVHAVW-----AGW-----GHAS 133  
Db 201 PAGLKKLIDASHQAGI-AVYLDVVYNHFGPDGNYNGQFGPYTSGSGTGWGDVVNINGHDS 259  
QY 134 ENPRLPESLAASKHKIIFIGPPG---SAMRSLGDKISSTIVAQAHDVPCMPWSGTG--- 186

Db 260 DEVR-NYILDAARQWFEFHV DGLRLDAVHSLDRGAYSLLAQLTMAEDVSAQTGIPRS 318  
Qy 187 -IKETMMSDQGLTVSD-----DVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGKG 239  
Db 319 LIAESELNDPKFVTSREAGGFLDAQWVDDIHHLHALVSGERNY-----YSDFGSVD 373  
Qy 240 IRKCTNGEEFKQL--YNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDC 297  
Db 374 LAK-TLREVFHTGNYSTYGRNHRPVH-PDITPASRFVYTTTHDQIGNR-AIGDRPS 430  
Qy 298 SVQRRHQKIIIEAPVTIAP-----ED 319  
Db 431 TTLTPEQQVLKAAIYSSPYTPMLFMGEEFGATPPAFFCSHTDPELNRLTSEGRKREFA 490  
Qy 320 RESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEF-----AFLELNPRLOVEHP--TTEM 371  
Db 491 RLGWNADDIPSELESTFTSSKLDWEFTAEOQRINDAYKQLHLRHTLGFSPNLLTLEV 550  
Qy 372 VSGVNIIPAAQLQVAMG----IPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTKPKQ 427  
Db 551 EHGEN----WLSMANGRILANFSDDTITV-----PLGGELI-YSFTSTVTDSTTLQ 600  
Qy 428 PQGHVVACR 436  
Db 601 PWGPAILTR 609

RESULT 38  
US-11-166-609-18  
; Sequence 18, Application US/11166609  
; Publication No. US20060015968A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBERTSEN, MARC C.  
; APPLICANT: FOX, TIM  
; APPLICANT: HUFFMAN, GARY  
; APPLICANT: TRIMNELL, MARY  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND  
; TITLE OF INVENTION: METHOD OF USING SAME  
; FILE REFERENCE: 1148CR  
; CURRENT APPLICATION NUMBER: US/11/166,609  
; PRIOR FILING DATE: 2005-06-24  
; PRIOR APPLICATION NUMBER: 10/412,000  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 09/670,153  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 18  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-11-166-609-18

Query Match 3.3%; Score 95.5; DB 7; Length 544;  
Best Local Similarity 19.7%; Pred. No. 5.6;  
Matches 103; Conservative 63; Mismatches 192; Indels 165; Gaps 24;  
Qy 15 NPLETAPASPVADFIRKQGGHVSITKVLICNNGI-----AAVKEI 54  
Db 3 SPMEEAHAMPVTSFFPVAGIHKLIAIFLVLSWILVHKWSLRNQKGRPSWPLIGATVEQL 62  
Qy 55 RSIRK---WAYETFGDERAI-----EFTVMATPEDLKNADYIRMADQYVEVPGGSNN 104  
Db 63 KNYHRMDLWVLEYSKDRVTVDMPFTSYTYIADP---VNVEHV-LKTNFTNYPKGEVY 117  
Qy 105 NNYANVDLIVDVAERAGVHAVW-----AGWGHASENPRLPESLAASKHKIIFIGPPGSA 158  
Db 118 RSYMDVLLGDGIFNADG--EMWRKORKTASFEPASKNLRDFSTVVFREYSLKLSSILSQA 175  
Qy 159 -----MRS LGDKISST-----IVAQHADV-----CMPWSGTGIKETM----- 191  
Db 176 CKAGRVVDMQELFMRTLDISICKVGFGEIGTSLSPDLPENSAFAQAFDAANIIVTLRFIDP 235

Qy 192 -----MSDQGLTVSDDVYQQACIHTAE-----EGLEKAEKIGYPVM---IK 230  
Db 236 LWRLKKFLHVGSEALLEQSMKLVDDFTYSVIRRRKAEILOARASGKQEKIKHDILSRFIE 295  
Qy 231 ASEGGGKGIRKCTNGEEF---KOLYNVAVLGEVPGS-----PVFVMK 269  
Db 296 LGEAGGDEG-----GGSGDDKSLRDVVLNFVIAGRDTTATLSWFTYMAMTHPAVADK 349  
Qy 270 LAGQARHLEVQ-----LLADQYGNA-----ISIFGRDCSVQRRHQKIIIEAPVT--- 313  
Db 350 LRRELAAFEDERAREEGVALADAGEASFAARVAQFASLLSYDAVGLVYLHACVTETLR 409  
Qy 314 ---IAPEDARESMEK-----AAVRLAKLVGYV--SAGTVEWLYSPESGEF----- 353  
Db 410 LYPVAVPQDPKGIVEDDDVLPDGTQVRAGGMVTYPYSGMRMEYNWGPDAASFRPERWLSGD 469  
Qy 354 --AFLELNPRLOVEHPTTEMVSGVNI---PAAQLQVAMGIPL 390  
Db 470 GGAFRNASP-----FKFTAFQAGPRICLGKDSAYLQMKMALAI 507

RESULT 39  
US-11-052-554A-8  
; Sequence 8, Application US/11052554A  
; Publication No. US20050288866A1  
; GENERAL INFORMATION:  
; APPLICANT: Sachdeva, et al.  
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL  
; FILE REFERENCE: 30853/40359A  
; CURRENT APPLICATION NUMBER: US/11/052,554A  
; CURRENT FILING DATE: 2005-02-07  
; PRIOR APPLICATION NUMBER: US 60/589,227  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
; PRIOR FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 763  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 1417  
; TYPE: PRT  
; ORGANISM: Escherichia coli 0157:H7  
US-11-052-554A-8

Query Match 3.3%; Score 95.5; DB 7; Length 1417;  
Best Local Similarity 23.5%; Pred. No. 22;  
Matches 64; Conservative 23; Mismatches 120; Indels 65; Gaps 11;  
Qy 231 ASEGGGKGIRKCTNGEEFKQLYNVAVLGEVPGSPVFMKLAGQ---ARHLEVQLLADQYG 287  
Db 731 AEGGSTAG---WTNNGDGTWTQAITLGTSTAGELEVMPKLNQNAANAANKVTWVAD--- 784  
Qy 288 NAISIFGRDCSVQRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGVVSAGTV--EWL 345  
Db 785 -ALSSNQSKVSAEDHVKAGESTTVTLVAKDAHGNAISGLALSASLTGTASEGATVSSW- 842  
Qy 346 YSPESGEFAF-----LELNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSI 393  
Db 843 --TEKNGSYVATLTGTGKTGELRVMLFNGQPAATE-----AAQLTVIAG-EMSSA 891  
Qy 394 RDIRLYGMDPRGNEVIDDFSSPESFQTKRKPOQGHVVACRITAEENPDGTGFKPG---- 449  
Db 892 NSTLVADNKAPTIVKTTTELTFTVXDAY-----GNPVTGLKPDAPVF 932  
Qy 450 MGALTELNFRSSSTSTWG-----YPSVGTSGA 475  
Db 933 SGAASTGSERPSPAGNWTGKNGVYVSTLTLS 964

RESULT 40  
US-11-070-080-16  
; Sequence 16, Application US/11070080  
; Publication No. US20050287625A1



; GENERAL INFORMATION:
; APPLICANT: Ye, Rick W.
; APPLICANT: Miller, Edward S.
; TITLE OF INVENTION: PROCESS FOR EXPRESSION OF FOREIGN GENES IN METHANE METABOLIZING
; BACTERIA THROUGH CHROMOSOMAL INTEGRATION
; FILE REFERENCE: CL-2443 US NA
; CURRENT APPLICATION NUMBER: US/11/070,080
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: US 60/550385
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Methylobionas sp. 16a
US-11-070-080-16

Query Match	3.3%	Score 95;	DB 7;	Length 423;
Best Local Similarity	21.1%	Pred. No. 4.2;		
Matches	66;	Conservative 57;	Mismatches 124;	Indels 66; Gaps 15;

  

QY	41	VLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNAD-YIRMADQYVEVP	99
Db	35	VVVCDECVELCNDI--IRD---ELAEDEKSVGSGALPKPKKEIKQELDNVYVIGQEKAKKIL	89
QY	100	GGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM	159
Db	90	SVAVYNHYKRL-----RSNSKKSDELAA--KSNILLIGPTGS--	124
QY	160	RLGDKISSTIVAQHADVPCMPWSGTGKETMMSDQGFLTVSDDVYQ-----QAC---	210
Db	125	---GKTLLEAETLARLLDVPF-----TIADATLTAEAGY--VGEDVENIIQKILQKCDYDV	174
QY	211	HTAEEGLEKAEKIGYPVMIKASEGGGKGIKCTNGEETFQLYNAVILGEVPGSPVFMKL	270
Db	175	EKAETGIVYIDEID-----KISRKADNPSTIRDSGEGVQQ---ALLKLIETVASVPPQ	226
QY	271	AGQARHLEVQLADQYGNASIF-----GRDCSVQRRHQKIIIEEAPVTIAPEDARESMEK	325
Db	227	GGR-KHPQQEFLQVNTANILFIVGGAFAGLDKVIKNRTEKGGIGFSAELKPKKEESQNVGE	285
QY	326	--AAVRLAKLVGY	336
Db	286	IFADVRAEDLIKY	298

Search completed: February 4, 2006, 18:28:59
Job time : 20 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:05:02 ; Search time 203 Seconds  
(without alignments)  
1209.915 Million cell updates/sec

Title: US-10-633-835-2  
Perfect score: 2907  
Sequence: 1 PPPDHKAVSQFIGNPLETA.....LDGLIQDRLTAERPPADLAV 559

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2874	98.9	559	ADJ47651	Adj47651 U. maydis
2	2222	76.4	2214	ADN10916	Adn10916 Phaffia r
3	2166	74.5	2273	AAR98811	Aar98811 Erysiphe
4	2163	74.4	591	ADJ47653	Adj47653 M. grisea
5	2139	73.6	2301	ADN21045	Adn21045 Bacterial
6	2079.5	71.5	2241	ADN19477	Adn19477 Bacterial
7	2061.5	70.9	2270	AAy24150	Aay24150 Candida a
8	2060	70.9	580	ADJ47654	Adj47654 S. cerevi
9	2060	70.9	2000	ABR52730	AbR52730 Protein s
10	2060	70.9	2000	ADK61968	AdK61968 Disease t
11	2060	70.9	2233	ADQ90738	Adq90738 Yeast ace
12	2060	70.9	2233	ADN19345	Adn19345 Bacterial
13	1889.5	65.0	983	ADN19252	Adn19252 Bacterial
14	1889.5	65.0	2000	ADK63986	AdK63986 Disease t
15	1790	61.6	632	ADJ47655	Adj47655 Human ACC
16	1787	61.5	2346	ADQ90744	Adq90744 Human ace
17	1781	61.3	2346	ABP70270	Abp70270 Amino aci
18	1781	61.3	2346	ABP59197	Abp59197 Human ace
19	1781	61.3	2346	ABP59195	Abp59195 Human ace
20	1781	61.3	2346	ABP59198	Abp59198 Human ace
21	1780	61.2	2348	ABH59490	Abh59490 Drosophil
22	1780	61.2	2348	AAO19075	Aao19075 Drosophil
23	1780	61.2	2348	ABB83866	Abb83866 Drosophil
24	1775	61.1	2288	AAB86033	Aab86033 Bovine ac

25	1774	61.0	2324	2	AAR05707	Aar05707 Acetyl-Co
26	1769.5	60.9	2420	8	ABM83569	Abm83569 Human dia
27	1769.5	60.9	2458	6	ABP59211	Abp59211 Human dru
28	1769.5	60.9	2487	6	ABB84649	Abb84649 Human SEC
29	1769.5	60.9	2498	5	ABU65149	Abu65149 Human NOV
30	1756.5	60.4	2498	8	ADN61949	Adn61949 Human nov
31	1738	59.8	774	8	ADJ47656	Adj47656 Human ACC
32	1697.5	58.4	2206	8	ADN03634	Adn03634 Antipsori
33	1669.5	57.4	2483	8	ADQ90746	Adq90746 Human ace
34	1669.5	57.4	2483	8	ADQ39507	Adq39507 Human myo
35	1669.5	57.4	2483	9	AEA33628	Aea33628 Human ACC
36	1604	55.2	555	8	ADJ47652	Adj47652 P. infest
37	1591.5	54.7	1096	8	ADQ39504	Adq39504 Human myo
38	1591.5	54.7	2486	4	AAU32848	Aau32848 Novel hum
39	1583	54.5	2240	2	AAR67819	Aar67819 Acetyl Co
40	1581.5	54.4	2359	5	ABB91251	Abb91251 Herbicida
41	1579	54.3	2204	3	AAG50615	Aag50615 Arabidops
42	1579	54.3	2243	8	ADN72177	Adn72177 Thale cre
43	1579	54.3	2254	2	AAR76949	Aar76949 ACCase. 2
44	1578	54.3	2254	2	AAV22129	Aay22129 Arabidops
45	1578	54.3	2254	2	AAV40598	Aay40598 Arabidops

ALIGNMENTS

RESULT 1  
ADJ47651.  
ID ADJ47651 standard; protein; 559 AA.  
XX AC ADJ47651;  
XX AC ADJ47651;  
DT 06-MAY-2004 (first entry)  
XX U. maydis ACCase BC domain SEQ ID NO:2.  
DE ACCase; Acetyl CoA carboxylase; carboxy transferase domain;  
KW biotin carboxylase domain; BC domain; fungicide.  
XX Ustilago maydis.  
OS WO2004013159-A2.  
PN 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024356.  
XX 05-AUG-2002; 2002US-0401170P.  
PR (CROP-) CROPSOLUTION INC.  
XX Ellich TD, Volrath SL, Weatherly SC;  
XX WPI; 2004-180421/17.  
XX Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted biotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase inhibitors/activators.  
XX Claim 8; SEQ ID NO 2; 56pp; English.  
XX The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxy transferase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in

CC an assay to detect inhibition or enhancement of Acetyl CoA carboxylase  
CC activity, and selecting a compound that inhibits or activates Acetyl CoA  
CC carboxylase activity. A peptide of the invention is also useful for  
CC identifying fungicides, which involves combining the peptide and a  
CC compound to be tested for the ability to bind to the biotin carboxylase  
CC domain, under conditions that permit binding to the biotin carboxylase  
CC domain, determining whether or not the compound binds to the biotin  
CC carboxylase domain, the presence of binding indicating the compound is or  
CC may be fungicide, employing the identified compound in an assay to detect  
CC inhibition of Acetyl CoA carboxylase activity, and selecting a compound  
CC that inhibits Acetyl CoA carboxylase activity. The present sequence  
CC represents an ACCase BC domain of the invention.  
XX  
SQ Sequence 559 AA;

Query Match 98.9%; Score 2874; DB 8; Length 559;  
Best Local Similarity 98.9%; Pred. No. 5.2e-261;  
Matches 553; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSVITKVLICNNGIAAVKEIRSIRKW 60  
Db 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSVITKVLICNNGIAAVKEIRSIRKW 60  
QY 61 AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERA 120  
Db 61 AYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERA 120  
QY 121 GVHAVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQAHDVPCM 180  
Db 121 GVHAVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQAHDVPCM 180  
QY 181 PWSGTGKETMMSDQGFLLTVSDDDVYQQACIHTAEEGLEKAEKIGYPYNIKASEGGGKGI 240  
Db 181 PWSGTGKETMMSDQGFLLTVSDDDVYQQACIHTAEEGLEKAEKIGYPYNIKASEGGGKGI 240  
QY 241 RKCTNGEEFKQLYNAVLEVPVSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300  
Db 241 RKCTNGEEFKQLYNAVLEVPVSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300  
QY 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
QY 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420  
Db 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420  
QY 421 KTQRKPQPOGHVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 421 KTQRKPQPOGHVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIKELSGDFTTVEYLIKLETDAPESNKITGWL 540  
Db 481 DSQFGHIFAYGADRSEARKQMVISLKELSIKELSGDFTTVEYLIKLETDAPESNKITGWL 540  
QY 541 DGLIQDRLTAERPPADLAV 559  
Db 541 DGLIQDRLTAERPPADLAV 559

RESULT 2  
ADN10916  
ID ADN10916 standard; protein; 2214 AA.  
XX  
AC ADN10916;  
XX  
DT 01-JUL-2004 (first entry)  
DE Phaffia rhodozyma acetyl-CoA carboxylase.  
XX  
KW Acetyl-CoA carboxylase; enzyme; astaxanthin; pigment; antioxidant.  
XX  
OS Xanthophyllomyces dendrorhous.

XX WO2004029232-A2.  
PN  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-EP010683.  
XX  
PR 27-SEP-2002; 2002EP-00021625.  
XX  
PA (STAM ) DSM IP ASSETS BV.  
XX  
PI Hoshino T, Ojima K, Setoguchi Y;  
XX  
DR WPI; 2004-329883/30.  
DR N-PSDB; ADN10914, ADN10915.  
XX  
PT New acetyl-CoA carboxylase polynucleotide derived from Phaffia rhodozyma  
PT or Xanthophyllomyces dendrorhous, useful for producing a recombinant  
PT vector or for increasing microbial production of carotenoids.  
XX  
PS Claim 1; SEQ ID NO 3; 82pp; English.  
XX  
CC The present sequence is the protein sequence of the acetyl-CoA  
CC carboxylase (ACC) gene of Phaffia rhodozyma (ATCC 74438). The sequence  
CC shows 56.28% amino acid sequence identity to a known ACC from Emericella  
CC nidulans. ACC is an enzyme involved in fatty acid biosynthesis. Its  
CC substrate is acetyl-CoA, which is also involved in the carotenogenic  
CC pathway of P. rhodozyma. A claimed method for producing ACC comprises  
CC culturing a recombinant organism containing a vector comprising an ACC  
CC polynucleotide. Also claimed is a recombinant organism in which gene  
CC expression of ACC is reduced as a result of antisense technology, site-  
CC directed mutagenesis, error-prone PCR or chemical mutagenesis. The  
CC recombinant organism is preferably P. rhodozyma or Xanthophyllomyces  
CC dendrorhous containing a vector comprising an antisense polynucleotide.  
CC It is used in a claimed process for producing carotenoids such as  
CC astaxanthin, beta-carotene, lycopene, zeaxanthin and canthaxanthin. The  
CC method is useful for increasing microbial production of carotenoids such  
CC as astaxanthin, which has antioxidant properties and is used as a  
CC colouring agent especially of farmed fish.  
XX  
SQ Sequence 2214 AA;

Query Match 76.4%; Score 2222; DB 8; Length 2214;  
Best Local Similarity 76.3%; Pred. No. 1.4e-198;  
Matches 424; Conservative 49; Mismatches 83; Indels 0; Gaps 0;  
QY 4 DHKAVSQFIGGNPLETAPASPVADFIKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYE 63  
Db 4 DHKAVSQFIGGNPLETAPASPVADFIKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYE 63  
QY 64 TFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERAGVH 123  
Db 64 TFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERAGVH 123  
QY 124 AVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQAHDVPCMPWS 183  
Db 124 AVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQAHDVPCMPWS 183  
QY 184 GTGKETMMSDQGFLLTVSDDDVYQQACIHTAEEGLEKAEKIGYPYNIKASEGGGKGIKRC 243  
Db 184 GTGKETMMSDQGFLLTVSDDDVYQQACIHTAEEGLEKAEKIGYPYNIKASEGGGKGIKRC 243  
QY 244 TNGEFKQLYNAVLEVPVSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRH 303  
Db 244 TNGEFKQLYNAVLEVPVSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRH 303  
QY 304 QKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQ 363  
Db 304 QKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQ 363  
QY 364 VEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQ 423  
Db 364 VEHPPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQ 423





CC carboxylase (ACCase) having a deleted biotin binding domain, having a  
CC deleted carboxy transferase domain, and having a functional biotin  
CC carboxylase domain. A peptide of the invention is useful for identifying  
CC Acetyl CoA carboxylase inhibitors or activators, which involves combining  
CC the peptide and a compound to be tested for the ability to bind to the  
CC biotin carboxylase domain, under conditions that permit binding to the  
CC biotin carboxylase domain, determining whether or not the compound binds  
CC to the biotin carboxylase domain, the presence of binding indicating the  
CC compound is or may be an Acetyl CoA carboxylase inhibitor or activator.  
CC The method further involves employing the identified binding compound in  
CC an assay to detect inhibition or enhancement of Acetyl CoA carboxylase  
CC activity, and selecting a compound that inhibits or activates Acetyl CoA  
CC carboxylase activity. A peptide of the invention is also useful for  
CC identifying fungicides, which involves combining the peptide and a  
CC compound to be tested for the ability to bind to the biotin carboxylase  
CC domain, under conditions that permit binding to the biotin carboxylase  
CC domain, determining whether or not the compound binds to the biotin  
CC carboxylase domain, the presence of binding indicating the compound is or  
CC may be fungicide, employing the identified compound in an assay to detect  
CC inhibition of Acetyl CoA carboxylase activity, and selecting a compound  
CC that inhibits Acetyl CoA carboxylase activity. The present sequence  
CC represents an ACCase BC domain of the invention.  
XX  
SQ Sequence 591 AA;

Query Match 74.4%; Score 2163; DB 8; Length 591;  
Best Local Similarity 73.5%; Pred. No. 5.4e-194;  
Matches 408; Conservative 59; Mismatches 88; Indels 0; Gaps 0;

QY 5 HKAVSQFIGGNPLETAPASPVADPIRKQGGHGVITKVLICNNGIAAVKEIRSIRKWAYET 64  
DB 37 HKIADHFIGGNPLETAPASPVADPIRKQGGHGVITKVLICNNGIAAVKEIRSIRKWAYET 96  
QY 65 FGDRAIEFTVMATPEDLKVNADYIRMDQYVEVPGSSNNNNYANVDLVDVAERAGVHA 124  
DB 97 FGDRAIQFTVMATPEDLQANADYIRMDHYVEVPGTNNNNYANVELVDVAERMNVHA 156  
QY 125 VWAGWGHASENPRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAQHADVPCMPWSG 184  
DB 157 VWAGWGHASENPKLPESLAASPKKIIFIGPPGSMRSLGDKISSTIVAQHAQVPCIPWSG 216  
QY 185 TGIKETMSDQGLTVSDDDVYQACIHTAEGLKAEKIGYPMIKASEGGGKGIKCT 244  
DB 217 TGVDVAVQIDKGIIVTDVDDTYAGCVTSWQEGLEKARQIGFPMIKASEGGGKGIKAV 276  
QY 245 NGEFQKLYNAVLEGEVPGSPVFMKLAGQARHLEVLQADQYGNALISIFGRDCSVQRRHQ 304  
DB 277 SEEGFEELYKAAASEIPGSPFIMKLAGNARHLEVLQADQYGNALISIFGRDCSVQRRHQ 336  
QY 305 KIIEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQV 364  
DB 337 KIIEAPVTIAPEDTFRKAMEEAAVRLGLVGYVSAGTVEYLYSHADDKFYFLELNPRLQV 396  
QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYISIRDIRLYGMDPRGNEVIDFDFSSPESFKTOR 424  
DB 397 EHPTTEGVSGVNLPSAQLIAMGIPLHRISDIRLLYGVDPKLSIDEIDFDFKPNPDSEKTOR 456  
QY 425 KPQPOGHVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOF 484  
DB 457 RPSPKGHLTACRITSEDPGEGFKPSNGVMHFNFRSSNVWGYFSVGTGQIHFSFSDSQF 516  
QY 485 GHIFAYGADRSEARKQWISLKELSIKIRGDFRTTVEYLIKLETDAFESNKITTGWLGLI 544  
DB 517 GHIFAYGENRSASRKHMVIALKELSIKIRGDFRTTVEYLIKLETEAFEENTITGWLDELI 576  
QY 545 QDRLTAERPPADLAV 559  
DB 577 SKLTAERPDKMLAV 591

RESULT 5  
ADN21045  
ID ADN21045 standard; protein; 2301 AA.

XX AC ADN21045;  
XX DT 02-DEC-2004 (first entry)  
XX DE Bacterial polypeptide #3698.  
XX KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX OS Bacteria.  
XX PN US2003233675-A1.  
XX PD 18-DEC-2003.  
XX PF 20-FEB-2003; 2003US-00369493.  
XX PR 21-FEB-2002; 2002US-0360039P.  
XX PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX PS Claim 1; SEQ ID NO 3698; 122pp; English.  
XX CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX SQ Sequence 2301 AA;

Query Match 73.6%; Score 2139; DB 8; Length 2301;  
Best Local Similarity 68.8%; Pred. No. 9.5e-191;  
Matches 411; Conservative 58; Mismatches 86; Indels 42; Gaps 2;

QY 5 HKAVSQFIGGNPLETAPASPVADPIRKQGGHGVIT-----KVLI 43





QY 488 PAYGADRSEARKQWVLSKELSGDFRTTVEYLKLETDAFESNKITTCGLDGLIQDR 547  
Db 481 FSFAESRESSRKSMVVALKELSGDFRTTVEYLVRLETKEFSENEFTTGWLDRLIAOK 540  
QY 548 LTAERPPADLAV 559  
Db 541 VTSARPDKMLAV 552

RESULT 7  
AAAY24150  
ID AAY24150 standard; protein; 2270 AA.  
XX  
AC AAY24150;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE Candida albicans acetyl CoA carboxylase.  
XX  
KW Candida albicans; acetyl CoA carboxylase; ACCase.  
XX  
OS Candida albicans.  
XX  
PN WO9932635-A1.  
XX  
PD 01-JUL-1999.  
XX  
PF 21-DEC-1998; 98WO-GB003857.  
XX  
PR 20-DEC-1997; 97GB-00026897.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Schnell NF, Dixon GK, Chavda S, Thain JL, Vincent JP;  
XX  
DR WPI; 1999-418931/35.  
DR N-PSDB; AAX88525.  
XX  
PT A polynucleotide encoding an Acetyl-CoA carboxylase gene from Candida  
PT albicans overexpressed in Saccharomyces cerevisiae for purification and  
PT isolation.  
XX  
PS Claim 7; Fig 5; 40pp; English.

XX The present sequence represents acetyl CoA carboxylase (ACCase) isolated  
CC from Candida albicans. The C. albicans ACCase is used in an assay to  
CC identify inhibitors of the enzyme. This is useful in pharmaceutical  
CC research. Inhibitors of ACCase are useful as antifungal agents. The  
CC invention also provides a novel expression system using Saccharomyces  
CC cerevisiae to express the C. albicans ACCase gene in quantifiable  
CC amounts. Expression of the C. albicans ACCase gene in S. cerevisiae  
CC overcomes prior art problems of isolation and purification of the ACCase.  
CC Controlled overexpression is used to improve expression of the ACCase. It  
CC is possible to achieve about 14-fold overexpression relative to the wild-  
CC type host S. cerevisiae strain JK9-3D. This is achieved by replacing the  
CC C. albicans promoter in the expression construct by a stronger and  
CC preferably inducible promoter such as the S. cerevisiae GAL1 promoter  
XX  
SQ Sequence 2270 AA;

Query Match 70.9%; Score 2061.5; DB 2; Length 2270;  
Best Local Similarity 70.7%; Pred. No. 1.9e-183;  
Matches 390; Conservative 63; Mismatches 98; Indels 1; Gaps 1;  
QY 9 SQFIGGNPLETAPSPVADFIRKQGGHSHVITKVLICNNGIAAIAVKEIRSKWAYETFGDE 68  
Db 70 SHFLGGNSVLNAEFSKVRDFVRAHQGHTVISKLIANNGIAAIAVKEIRSKWAYETFGDE 129  
QY 69 RAIEFTVMATPEDLVNADYIRMDQYVEVPGGSNNNNYANVDLIVDAERAGVHAVWAG 128  
Db 130 KAIQFTVMATPEDLEANAIEYIRMDQFIEVPGGTNNNNYANVDLIVEIAESTNAHAVWAG 189

QY 129 WGHASENPRLPESLAASKHKIIFIGPPGSGAMRSLGDKISSTIVAQAHDVPCMPWSGTGIK 188  
Db 190 WGHASENPRLPEKLAASPKKIIFIGPPGSGAMRSLGDKISSTIVAQAHDVPCIPWSGTGVD 249  
QY 189 ETWMSDQ-GFLTVDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGE 247  
Db 250 EVKIDPQTNLVSADDIYAKGCCTSPEDGLEKAKKIGFPVMIKASEGGGKGIRKVDDEK 309  
QY 248 EFKQLYNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKII 307  
Db 310 NFITLYNQAANEIPGSPIFIMKLAGDARHLEVQLLADQYGNALISIFGRDCSVQRRHQKII 369  
QY 308 EEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVWLYSPESGEFAPLELNPRLQVEHP 367  
Db 370 EEAPVTIARKETFEHMEANAARVLGKLVGYVSAGTVWLYSHAEKDFYFLELNPRLQVEHP 429  
QY 368 TTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTKQKPQ 427  
Db 430 TTEMVTGVNLPAAQLQIAMGIPMHRIRDIRTYGADPHTTTIDDFEFSKSETSLVSQRRPT 489  
QY 428 PQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGVGTSGALHEYADSQFGHI 487  
Db 490 PKGHCTACRITSEDPGEGFKPSCGSLHELNFRSSNVWGYFSGVGNQSSIHFSFSDSQFGHI 549  
QY 488 FAYGADRSEARKQWVLSKELSGDFRTTVEYLKLETDAFESNKITTCGLDGLIQDR 547  
Db 550 FAFGENRQASRKHMVVALKELSGDFRTTVEYLKLETDAFEDNTTITGWLDELITKK 609  
QY 548 LTAERPPADLAV 559  
Db 610 LTAERPDPIVAV 621

RESULT 8  
ADJ47654  
ID ADJ47654 standard; protein; 580 AA.  
XX  
AC ADJ47654;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE S. cerevisiae ACCase BC domain SEQ ID NO:8.  
XX  
KW ACCase; Acetyl CoA carboxylase; carboxy transferase domain;  
KW biotin carboxylase domain; BC domain; fungicide.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO2004013159-A2.  
XX  
PD 12-FEB-2004.  
XX  
PF 04-AUG-2003; 2003WO-US024356.  
XX  
PR 05-AUG-2002; 2002US-0401170P.  
XX  
PA (CROP-) CROPSOLUTION INC.  
XX  
PI Elich TD, Volrath SL, Weatherly SC;  
XX  
DR WPI; 2004-180421/17.

XX Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted  
PT biotin binding domain and carboxy transferase domain, and having  
PT functional biotin carboxylase domain, useful for identifying ACCase  
PT inhibitors/activators.  
XX  
PS Claim 9; SEQ ID NO 8; 56pp; English.  
XX  
CC The invention relates to a novel peptide (I) comprising an acetyl CoA  
CC carboxylase (ACCase) having a deleted biotin binding domain, having a  
CC deleted carboxy transferase domain, and having a functional biotin  
CC carboxylase domain. A peptide of the invention is useful for identifying

CC Acetyl CoA carboxylase inhibitors or activators, which involves combining  
CC the peptide and a compound to be tested for the ability to bind to the  
CC biotin carboxylase domain, under conditions that permit binding to the  
CC biotin carboxylase domain, determining whether or not the compound binds  
CC to the biotin carboxylase domain, the presence of binding indicating the  
CC compound is or may be an Acetyl CoA carboxylase inhibitor or activator.  
CC The method further involves employing the identified binding compound in  
CC an assay to detect inhibition or enhancement of Acetyl CoA carboxylase  
CC activity, and selecting a compound that inhibits or activates Acetyl CoA  
CC carboxylase activity. A peptide of the invention is also useful for  
CC identifying fungicides, which involves combining the peptide and a  
CC compound to be tested for the ability to bind to the biotin carboxylase  
CC domain, under conditions that permit binding to the biotin carboxylase  
CC domain, determining whether or not the compound binds to the biotin  
CC carboxylase domain, the presence of binding indicating the compound is or  
CC may be fungicide, employing the identified compound in an assay to detect  
CC inhibition of Acetyl CoA carboxylase activity, and selecting a compound  
CC that inhibits Acetyl CoA carboxylase activity. The present sequence  
CC represents an ACCase BC domain of the invention.  
XX  
SQ Sequence 580 AA;

Query Match 70.9%; Score 2060; DB 8; Length 580;  
Best Local Similarity 69.1%; Pred. No. 2.6e-184;  
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;  
QY 3 PDHKAVSQFIGGNPLETAPASPVPADFIKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAY 62  
Db 28 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSIRKWAY 82  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIARMADQYVEVPGGSSNNNNYANVDLIVDVAERAGV 122  
Db 83 ETFGDDRTVQFVAMATPEDLEANAIEYIARMADQYIEVPGGTTNNNNYANVDLIVDIAERADV 142  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQHADVPCMPW 182  
Db 143 DAVWAGWGHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSSTIVAQSAKVPCIPW 202  
QY 183 SGTGIKETMMSDQ--GFLTVDVDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240  
Db 203 SGTGV-DTVHVDEKTLGLSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 261  
QY 241 RKCTNGEEFKQLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300  
Db 262 RQVEREEDFIALYHQAAANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGDCSVQ 321  
QY 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 322 RRHQKIIIEEAPVTIAKAETFHEMEKAAVRLGKLVGYVSAGTVEYLYSHDDGKGFYFLELNP 381  
QY 361 RLQVEHPTTEMVSGVNPAAQLQVAMGIPLYSIRDITRTLYGMDPRGNEVIDDFSSPESF 420  
Db 382 RLQVEHPTTEMVSGVNPAAQLQIAMGIPMHRISDIRTLTYGMNPHSASEIDFEFTQDAT 441  
QY 421 KTQRKPOQGHVVACRITAENPDGTGKPGMGALTELNFRSSTSTWGYSFVGTSGALHEYA 480  
Db 442 KKQRRPIPKGHTACRITSEDPNDGFKPSGGTLHELNFRSSSNWGYFSVGNNGNIHSFS 501  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLYLKLLETDAFESNKITTGWL 540  
Db 502 DSQFGHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLYLKLLETFEDFEDNTITTGWL 561  
QY 541 DGLIQRDLTAERPPADLAV 559  
Db 562 DLLITHKMTAEKPDPTLAV 580

RESULT 9  
ABR52730  
ID ABR52730 standard; protein; 2000 AA.

XX  
AC ABR52730;  
XX

DT 20-JUN-2003 (first entry)  
XX  
DE Protein sequence #SEQ ID 325.  
XX  
KW Multiprotein complex; eukaryote; drug target; diagnosis.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN EPI258494-A1.  
XX  
PD 20-NOV-2002.  
XX  
PF 20-DEC-2001; 2001EP-00130253.  
XX  
PR 15-MAY-2001; 2001EP-00111774.  
XX  
PA (CELL-) CELLZOME AG.  
XX  
PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;  
PI Marzioch M, Schultz JD, Superti-Furga GD;  
XX  
DR WPI; 2003-250078/25.  
XX N-PSDB; ACC60772.  
PT New isolated protein complexes useful for diagnosing a disease or  
PT disorder, or as a target for an active agent of a pharmaceutical,  
PT preferably a drug target in the treatment or prevention of disease or  
XX disorder.  
PS Disclosure; SEQ ID NO 325; 17pp + Sequence Listing; English.  
XX  
CC The invention relates to multiprotein complexes from eukaryotes. Proteins  
CC of the invention and DNA sequences encoding them are given in records  
CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are  
CC obtainable by using a protein as a bait and isolating the set of proteins  
CC which is attached thereto from cells. Such protein complexes may comprise  
CC up to 30 distinct proteins. Protein complexes of the invention are useful  
CC for diagnosing a disease or disorder, or as a target for an active agent  
CC of a pharmaceutical, preferably a drug target in the treatment or  
CC prevention of a disease or disorder. Note: The sequence data for this  
CC patent is not represented in the printed specification, but is based on  
CC sequence information supplied by the European Patent Office. The complete  
CC document is available on CD-ROM  
XX  
SQ Sequence 2000 AA;

Query Match 70.9%; Score 2060; DB 6; Length 2000;  
Best Local Similarity 69.1%; Pred. No. 2.1e-183;  
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;  
QY 3 PDHKAVSQFIGGNPLETAPASPVPADFIKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAY 62  
Db 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSIRKWAY 83  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIARMADQYVEVPGGSSNNNNYANVDLIVDVAERAGV 122  
Db 84 ETFGDDRTVQFVAMATPEDLEANAIEYIARMADQYIEVPGGTTNNNNYANVDLIVDIAERADV 143  
QY 123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSSTIVAQHADVPCMPW 182  
Db 144 DAVWAGWGHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSSTIVAQSAKVPCIPW 203  
QY 183 SGTGIKETMMSDQ--GFLTVDVDDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240  
Db 204 SGTGV-DTVHVDEKTLGLSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 262  
QY 241 RKCTNGEEFKQLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300  
Db 263 RQVEREEDFIALYHQAAANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGDCSVQ 322  
QY 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 323 RRHQKIIIEEAPVTIAKAETFHEMEKAAVRLGKLVGYVSAGTVEYLYSHDDGKGFYFLELNP 382





10-JAN-2003; 2003US-0439383P.  
31-MAR-2003; 2003US-0459464P.  
31-JUL-2003; 2003US-0491640P.  
27-OCT-2003; 2003US-0514636P.  
09-JAN-2004; 2004US-00514636.  
(UYCO ) UNIV COLUMBIA NEW YORK.  
Tong L, Zhang H, Yang Z;  
WPI; 2004-571486/55.  
New crystallizable composition comprising a carboxyltransferase domain of acetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes, obesity, cardiovascular disease, atherosclerosis, or cancer.  
Example 4; SEQ ID NO 1; 195pp; English.  
The invention comprises a crystallisable composition containing a carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA) carboxylase. The composition of the invention is useful for treating: metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia, hypertension, hyperuricaemia and renal dysfunction. The present amino acid sequence represents a yeast acetyl-CoA carboxylase of the invention.  
Sequence 2233 AA;  
Query Match 70.9%; Score 2060; DB 8; Length 2233;  
Best Local Similarity 69.1%; Pred. No. 2.5e-183;  
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;  
3 PDHKAVSQFIGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAVKEIRSIRKWAY 62  
29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSIRKWAY 83  
63 ETFGDERAIEFTVMATPEDLVKNADYIRMDQYVEVPGSGNNNNYANVDLIVDVAERAGV 122  
84 ETFGDDRTVQFVAMATPEDLEANAIEYIRMDQYIEVPGGTNNNNYANVDLIVDIAERADV 143  
123 HAVWAGWGCHASENRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 182  
144 DAVWAGWGCHASENPLLPKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVAQAQKVPCTIPW 203  
183 SGTGKETMMSDQ--GFLTVDVYQQACIHTAEGLKAEKIGYPMIKASEGGGKGI 240  
204 SGTGV-DTVHVDEKTLVSVDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 262  
241 RKTNGEEFKQLYNAVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQ 300  
263 RQVEREEDFIALYHQAAEIPGSPIFIMKLAGRARHLEVQLLADQYGTNISLFGKDCSVQ 322  
301 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVWLYSPESGEFAFLELNP 360  
323 RRHQKIIIEAPVTIAKAEETHMEKAAVRLKLVGYVSAGTVVEYLYSHDDGKFYFLELNP 382  
361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFSSPESF 420  
383 RLQVEHPTTEMVSGVNLPAALQIAQIAMPIMHRISDIRTLTYGMNPHSASEIDPFKTDAT 442  
421 KTQRKPOQGHVVACRITAENPDGTGKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
443 KKQRRPIPKGHCTACRITSEDNDGFKPSGGTLHELNFRSSSNWGYFSVGNNGNIHSFS 502  
481 DSQFGHIFAYGADRSEARKQMWISLKELSIRGDFRTVEYLYKLLETDAFESNKITTGWL 540  
503 DSQFGHIFAFGENRQSRKHMVVALKELSIRGDFRTVEYLYKLLETDFEDNTITGWL 562  
541 DGLIQDRLTAERPPADLAV 559  
563 DDLITHKMTAEKPDPTLAV 581

RESULT 12  
ADN19345  
ID ADN19345 standard; protein; 2233 AA.  
XX  
AC ADN19345;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #1998.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
DR WPI; 2004-061375/06.  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 1998; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 2233 AA;

Query Match 70.9%; Score 2060; DB 8; Length 2233;

Best Local Similarity 69.1%; Pred. No. 2.5e-183;  
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;  
QY 3 PDHKAVSQFIGGNPLETAPASPVDPIRKOQGHSHVITKVLICNNGIAAAVKEIRSIRKWA 62  
Db 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAAVKEIRSIRKWA 83  
QY 63 ETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDVAERAGV 122  
Db 84 ETFGDDRTVQFVAMATPEDLEANAIEYIRMAQYIEVPGGTNNNNYANVDLIVDIAERADV 143  
QY 123 HAVWAGWGHAENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMPW 182  
Db 144 DAVWAGWGHAENRPLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSITIVAQSAKVPCIPW 203  
QY 183 SGTGIKETMMSDQ--GFLTVDVYQACIHTAEGLKAEKIGYPMIKASEGGGKG 240  
Db 204 SGTGV-DTVHVDKTLGVSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKG 262  
QY 241 RKCTNGEEFKQLYNVNLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300  
Db 263 RQVEREEDFIALYHOAANEIPGSPIFIMKLAGRAHLEVQLLADQYGTNLSLFGRDQSVQ 322  
QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360  
Db 323 RRHQKIIIEAPVTIAKAEFTHEMEKAAVRLKLVGYVSAGTVEYLYSHDDGKFYFLELNP 382  
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDESSPESF 420  
Db 383 RLQVEHPTTEMVSGVNLPAALQIAMIPIHRSIDITLYGMNPHSASEIDFEFTQDAT 442  
QY 421 KTQRKPOQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480  
Db 443 KKQRRPIPKGHCTACRITSEDPNDGFKPSGGTTLHNLNFRSSNVWGYFSVGNNGNIHSFS 502  
QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIIRGDFRTVEYLIKLETDAPESNKITGWL 540  
Db 503 DSQFGHIFAFGENQASRKHMVVALKELSIIRGDFRTVEYLIKLETFEDNTITGWL 562  
QY 541 DGLIQDRLTAERPPADLAV 559  
Db 563 DDLITHKMTAEKPDPTLAV 581

RESULT 13  
ADN19252  
ID ADN19252 standard; protein; 983 AA.  
XX AC ADN19252;  
XX DT 02-DEC-2004 (first entry)  
XX DE Bacterial polypeptide #1905.  
XX KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX OS Bacteria.  
XX PN US2003233675-A1.  
XX PD 18-DEC-2003.  
XX PF 20-FEB-2003; 2003US-00369493.  
XX PR 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
PT  
XX  
PS Claim 1; SEQ ID NO 1905; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 983 AA;

Query Match 65.0%; Score 1889.5; DB 8; Length 983;  
Best Local Similarity 64.3%; Pred. No. 7.3e-168;  
Matches 355; Conservative 86; Mismatches 94; Indels 17; Gaps 4;

QY 2 PPDHKAVSQFIGGNPLETAPASPVDPIRKOQGHSHVITKVLICNNGIAAAVKEIRSIRKWA 61  
Db 105 PP-----QFIGLNTVESAQPSILRDFVLRGGHTVISKILIANNGIAAAVKEIRSIRKWA 158  
QY 62 YETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDVAERAG 121  
Db 159 YETFNDEKIIQFVVMATPDDLHANSEYIRMAQYVQVPGGTNNNNYANIDLILDVAEQTD 218  
QY 122 HAVWAGWGHAENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSITIVAQHADVPCMP 181  
Db 219 VDAVWAGWGHAENRPLPELLASSQKILFIGPPGRAMRSLGDKISSITIVAQSAKIPCI 278  
QY 182 WSGTGIKETMMSDQ--GFLTVDVYQACIHTAEGLKAEKIGYPMIKASEGGGKG 239  
Db 279 WSGSHI-DTIHIDNKTNFVSPDDVYVVGCCSSPEDALEKAKLIGFPVMIKASEGGGKG 337  
QY 240 IRKCTNGEEFKQLYNVNLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSV 299  
Db 338 IRRVDNEDDFIALYRQAVNETPGSPFMVKVVTDAHLEVQLLADQYGTNITLFGRDCSI 397  
QY 300 QRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELN 359  
Db 398 QRRHQKIIIEAPVTITKPTFORMERAARLGLVGYVSAGTVEYLYSPKDDKFYFLELN 457  
QY 360 PRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDESSPES 419  
Db 458 PRLQVEHPTTEMISGVNLPATQLQIAMGIPMHMISDIRKLYGLDPTGTYSID----- 509

QY 420 FKTQKPKPOGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEY 479  
DB 510 FKNLKRPSPKGHCISCRTSEDPNEGFKPSTGKIHELNFRSSNVWGYFSGVNGAIHSF 569  
QY 480 ADSQFGHIFAYGADRSEARKQMVISLKELSGIRGDFRTTVEYLKLETDAFESNKITGW 539  
DB 570 SDSQFGHIFAVGNDRQDAKQNMVLALKDIFSIRGEFKTPIEYLIELLETRDFESNNISTGW 629  
QY 540 LDGLIQDRLTAE 551  
DB 630 LDDLILKNLSSD 641

RESULT 14  
ADK63986  
ID ADK63986 standard; protein; 2000 AA.  
AC ADK63986;  
XX  
DT 06-MAY-2004 (first entry)  
DE Disease treating protein complex-derived protein #1382.  
XX

KW protein complex; drug target; diagnosis.  
XX  
OS Unidentified.  
XX  
PN EP1338608-A2.  
XX  
PD 27-AUG-2003.  
XX  
PF 20-DEC-2002; 2002EP-00102902.  
XX  
PR 20-DEC-2001; 2001EP-00130253.  
XX  
PA (CELL-) CELLZOME AG.  
XX  
PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;  
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
PI Michon A, Leutwein C, Rick J;  
XX  
DR WPI; 2003-638460/61.  
DR N-PSDB; ADK63987.

PT New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.

PS Disclosure; SEQ ID NO 2763; 13pp; English.

XX  
XX The invention relates to novel protein complexes comprising a first and a  
CC second protein, or its derivative, fragment, homologue or variant. The  
CC proteins are selected from given protein complexes, which are not defined  
CC in the specification. The variants are encoded by nucleic acids that  
CC hybridize to the nucleic acids encoding the proteins under low stringency  
CC conditions. The protein complexes are useful as targets for an active  
CC agent of a pharmaceutical. These protein complexes are particularly  
CC useful as drugs targets for the treatment or preventing of a disease or  
CC disorder. The complexes and methods above are useful in diagnosing or  
CC screening for the presence of a disease or disorder or a predisposition  
CC for developing a disease or disorder in a subject. These are also useful  
CC in screening for a drug for treatment or prevention of a disease or  
CC disorder. The molecule that modulates the amount, activity or protein  
CC components of the complex is useful for the manufacture of a medicament  
CC for the treatment or prevention of a disease or disorder. This sequence  
CC corresponds to a protein of the invention. (Note: the sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained from the EPO in electronic format).

XX Sequence 2000 AA;

Query Match 65.0%; Score 1889.5; DB 7; Length 2000;  
Best Local Similarity 64.3%; Pred. No. 2.4e-167;  
Matches 355; Conservative 86; Mismatches 94; Indels 17; Gaps 4;  
QY 2 PPHKAVSQFIGGNPLETASPVPADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWA 61  
DB 105 PP-----QFIGLNTVESAQPSILRDFVDRGGHTVISKILIANNGIAAVKEMRSIRKWA 158  
QY 62 YETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVPGGSSNNNYANVDLIVDVAERAG 121  
DB 159 YETFNDEKIIQFVVMATPDDLHANSEYIRMAQYVQVPGGTNNNYANIDLILDVAEQTD 218  
QY 122 VHAWAGWGHAHENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMP 181  
DB 219 VDAVWAGWGHAHENPCLPELLASSQKILFIGPPGRAMRSLGDKISSTIVAQSAKIPICP 278  
QY 182 WSGTGIKETMMSDQ--GFLTVDSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKG 239  
DB 279 WSGSHI-DTIHIDNKTNFVSPDDVYVVGCCSSPEDALEKAKLIGFPMIKASEGGGKG 337  
QY 240 IRKCTNGEEFKQLYNAVLEVPSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSV 299  
DB 338 IRRVDNEDDFIALYRQAVNETPGSPFMFVMKVVTDAHLEVQLLADQYGTNITLFGRDCSI 397  
QY 300 QRRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLVSPEGEFAFLELN 359  
DB 398 QRRHQKIIIEAPVTITKPTFQRMERAAIRLGELVGYVSAGTVEYLYSPKDDKFYFLELN 457  
QY 360 PRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTYGMDPRGNEVIDDFSSPES 419  
DB 458 PRLQVEHPTTEMISGVNLPATQLQIAMGIPMHMISDIRKLYGLDPTGTSYID----- 509  
QY 420 FKTQKPKPOGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEY 479  
DB 510 FKNLKRPSPKGHCISCRTSEDPNEGFKPSTGKIHELNFRSSNVWGYFSGVNGAIHSF 569  
QY 480 ADSQFGHIFAYGADRSEARKQMVISLKELSGIRGDFRTTVEYLKLETDAFESNKITGW 539  
DB 570 SDSQFGHIFAVGNDRQDAKQNMVLALKDIFSIRGEFKTPIEYLIELLETRDFESNNISTGW 629  
QY 540 LDGLIQDRLTAE 551  
DB 630 LDDLILKNLSSD 641

RESULT 15  
ADJ47655  
ID ADJ47655 standard; protein; 632 AA.  
XX  
AC ADJ47655;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human ACC1 BC domain SEQ ID NO:10.  
XX  
KW ACCase; Acetyl CoA carboxylase; carboxy transferase domain;  
KW biotin carboxylase domain; BC domain; fungicide; human; ACC1.  
XX  
OS Homo sapiens.  
XX  
PN WO2004013159-A2.  
XX  
PD 12-FEB-2004.  
XX  
PF 04-AUG-2003; 2003WO-US024356.  
XX  
PR 05-AUG-2002; 2002US-0401170P.  
XX  
PA (CROP-) CROPSOLUTION INC.  
XX  
PI Elich TD, Volrath SL, Weatherly SC;  
XX  
DR WPI; 2004-180421/17.





Db 222 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGITPLPWSGSLRVDWQENDFSKRIL 279  
Qy 199 TVSDDVYQACIHTAEGLKEAEKIGYPMVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258  
Db 280 NVPQELYEKGYVKDVGDDGLQAAEEVGYPMVMIKASEGGGKGIRKVNADDFPNLFRQVQA 339  
Qy 259 EVPGPSVFMVMIKAGQARHLEVQLLADQYGNALISIFGRDCSVQRHQRHKKIIEEAPVTIAPED 318  
Db 340 EVPGPSPIFVMRLAKQSRHLEVQLLADQYGNALISLFGSDCSVQRHQRHKKIIEEAPATIATPA 399  
Qy 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378  
Db 400 VFEHMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLQVEHPTTEMVADVNL 458  
Qy 379 AAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDDFSSPESFQTKRQKPOQGHVACRIT 438  
Db 459 AAQLQIAMGIPLYRIKDIRMMYGVSPWGDSPIDFDSA-----HVPCEPRGHVIAARIT 511  
Qy 439 AENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498  
Db 512 SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGLHEFADSQFGHCFSGWGENREEAI 571  
Qy 499 KOMVISLKELSIKIRGDFRTTVEYLYKLLETDAFESNKITTTGWLGLIQDRLTAERPPADLA 558  
Db 572 SNMVVALKELSIKIRGDFRTTVEYLYKLLETESFQMNRIIDTGWLDRLIAEKVQAERPD 631  
Qy 559 V 559  
Db 632 V 632

RESULT 17

ABP70270  
ID ABP70270 standard; protein; 2346 AA.

XX AC ABP70270;

XX DT 07-APR-2003 (first entry)

XX DE Amino acid sequence of human acetyl coenzyme A-carboxylase alpha.

XX KW Acetyl coenzyme A-carboxylase alpha; ACC-alpha; BRCA1; breast cancer;

XX KW ovarian cancer.

XX OS Homo sapiens.

XX PN WO2002100897-A2.

XX PD 19-DEC-2002.

XX PF 12-JUN-2002; 2002WO-FR002016.

XX PR 13-JUN-2001; 2001FR-00007740.

XX PR 05-MAR-2002; 2002FR-00002789.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.

XX PI Dalla Venezia N, Magnard C, Lenoir G, Sinilnikova-Erard O;

XX DR WPI; 2003-148772/14.

XX DR N-PSDB; AB223503.

XX PT New molecular complex of BRCA1 protein and acetyl coenzyme A-carboxylase

XX PT alpha, useful in screening agents suitable for treatment, prevention or

XX PT diagnosis of cancer.

XX PS Disclosure; Page 55-62; 62pp; French.

XX CC

XX CC The present sequence represents human acetyl coenzyme A-carboxylase alpha

XX CC (ACC-alpha). The ACC-alpha protein was used in the course of the

XX CC invention. The specification describes a molecular complex comprising a

XX CC polypeptide having amino acids 1640-1663 of the human BRCA1 protein (or

CC similar sequence from some other animal species), and a polypeptide that  
CC is a part of the acetyl coenzyme A-carboxylase alpha (ACC-alpha) protein  
CC able to bind the BRCA1 protein. The complex is implicated in  
CC predisposition to cancer of breast and ovary. It is used to screen for  
CC compounds that modulate interaction between BRCA1 and ACC-alpha, which  
CC are potentially useful for treatment, prevention and diagnosis of cancer,  
CC and to identify endogenous ligands. Modulated formation of the complex  
CC can be used for diagnosis of cancer. Antibodies directed against specific  
CC parts of human ACC-alpha are useful for localization of the complex in  
CC cells

XX SQ Sequence 2346 AA;

Query Match 61.3%; Score 1781; DB 6; Length 2346;  
Best Local Similarity 63.6%; Pred. No. 5.2e-157;  
Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

Qy 22 ASPVADFIRKQGHSVITKVLICNNGIAAANKVIRSRIRKWAYETFGDERAIEFTVMATPED 81  
Db 103 ASP-AEFTVTRFGGNKVKIEKVLIANNGIAAANKVIRSRIRSRNERNERAIRFVVMVTPED 161

Qy 82 LKVNADYIRMAQYVEVPGSGNNNNYANVDLIIVDAERAGVHAVWAGWGHASENPRLPES 141

Db 162 LKANAERYIKMAADHYVPVPGGANNNNYANVELLIDIAKRIPVQAVWAGWGHASENPKLP 221

Qy 142 LAASKHKIIFIGPGSAMRSLGDKISSITVAQHADVPCMPWSGTGIKETMTSD---QGFL 198

Db 222 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGITPLPWSGSLRVDWQENDFSKRIL 279

Qy 199 TVSDDVYQACIHTAEGLKEAEKIGYPMVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258

Db 280 NVPQELYEKGYVKDVGDDGLKAAEKVGYPMVMIKASEGGGKGIRKVNADDFPNLFRQVQA 339

Qy 259 EVPGPSVFMVMIKAGQARHLEVQLLADQYGNALISIFGRDCSVQRHQRHKKIIEEAPVTIAPED 318

Db 340 EVPGPSPIFVMRLAKQSRHLEVQLLADQYGNALISLFGSDCSVQRHQRHKKIIEEAPATIATPA 399

Qy 319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378

Db 400 VFEHMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLQVEHPTTEMVADVNL 458

Qy 379 AAQLQVAMGIPLYSIIRDITLYGMDPRGNEVIDDFSSPESFQTKRQKPOQGHVACRIT 438

Db 459 AAQLQIAMGIPLYRIKDIRMMYGVSPWGDSPIDFENSA-----HVPCEPRGHVIAARIT 511

Qy 439 AENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498

Db 512 SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGLHEFADSQFGHCFSGWGENREEAI 571

Qy 499 KOMVISLKELSIKIRGDFRTTVEYLYKLLETDAFESNKITTTGWLGLIQDRLTAERPPADLA 558

Db 572 SNMVVALKELSIKIRGDFRTTVEYLYKLLETESFQMNRIIDTGWLDRLIAEKVQAERPD 631

Qy 559 V 559

Db 632 V 632

RESULT 18

ABP59197

ID ABP59197 standard; protein; 2346 AA.

XX AC ABP59197;

XX DT 01-MAY-2003 (first entry)

XX DE Human acetyl-Coenzyme A-carboxylase-alpha variant #1.

XX KW Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;

XX KW breast; ovary.

XX OS Homo sapiens.

FH	Key	Location/Qualifiers	
FT	Misc-difference 1405	/note= "Leu substituted with Val"	
FT			
XX			
PN	WO2002100896-A2.		
XX			
PD	19-DEC-2002.		
XX			
PF	12-JUN-2002; 2002WO-FR002015.		
XX			
PR	13-JUN-2001; 2001FR-00007740.		
PR	05-MAR-2002; 2002FR-00002788.		
XX			
PA	(CNRS ) CNRS' CENT NAT RECH SCI.		
PA	(UYLY-) UNIV LYON 1 BERNARD CLAUDE.		
XX			
PI	Dalla Venezia NL, Magnard CM, Lenoir GM, Sinilnikova-Erard O;		
XX			
DR	WPI; 2003-175165/17.		
XX			
PT	In vitro diagnosis of cancer, particularly breast and ovarian cancer, or		
PT	susceptibility, comprises detecting alterations in the acetyl coenzyme A-		
PT	carboxylase alpha gene or protein expression.		
XX			
PS	Example 2; Page: 56pp; French.		
XX			
CC	The present sequence is a variant sequence for human acetyl-Coenzyme A-		
CC	carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro		
CC	diagnosis of cancer (or of an increased risk of developing it), by		
CC	detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha		
CC	protein expression, relative to a control population. The method is		
CC	particularly used to diagnose cancer, especially of breast or ovary, or		
CC	for assessing the risk of developing such cancers. Note: The present		
CC	sequence was not shown in the specification, but was derived from		
CC	information given		
XX			
SQ	Sequence 2346 AA;		
Query Match 61.3%; Score 1781; DB 6; Length 2346;			
Best Local Similarity 63.6%; Pred. No. 5.2e-157;			
Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;			
Qy	22	ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED	81
Db	103	ASP-AEFVTRFGGNKVIEKVLIANNGIAAVKCMRSIRRSWSEYEMFRNERAIRFVVMVTPED	161
Qy	82	LKVNADYIRMADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES	141
Db	162	LKANAEYIKWADHYVPVPGGANNNNYANVELILDIAKRIPQAVWAGWGHASENPKLPPEL	221
Qy	142	LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---	QGFL 198
Db	222	LL--KNGIAFMGPPNQAMWALGDKIASSIVAQTAGITPLPWSGSLRVWDQENDFSKRIL	279
Qy	199	TVSDDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLG	258
Db	280	NVPQELYEKGYVKDVGGLKAAEKVGYPMIKASEGGGKGIRKVNADDPPNLFROVQA	339
Qy	259	EVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEAPVTIAPED	318
Db	340	EVPGSPIFVMRLAKQSRHLEVQILADQYGNALISLFGDCSVQRHOKIIEEAPATIATPA	399
Qy	319	ARESMKAAVRLAKLVGYVSAGTVWELVSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP	378
Db	400	VFEHMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLQVEPCTEMVADVNL	458
Qy	379	AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSPSPESFKTKRQKPQGHVACRIT	438
Db	459	AAQLQIAMGIPLYRIKDIRMYGVSPWGSPIDFENSA-----HVP CPRGHVIAARIT	511
Qy	439	AENPDTGFKPCMGALTELNFRSSSTSTWGYFSVGTSGALHEYADSQGHIFAYGADRSEAR	498
Db	512	SENPDGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFAGSQGHCFSGWGENREEAI	571
Qy	499	KQMVISLKELSGRDFRTTVEYLIKLLEDAFESNKITTGWLDGLIQDRLTAERPAPDLA	558
Db	572	SNMVVALKELSGRDFRTTVEYLIKLLETESFQMNRI DTGWLDRLIAEKVRAERPDTMDG	631
Qy	559	V 559	
Db	632	V 632	
RESULT 19			
ABP59195			
ID	ABP59195	standard; protein; 2346 AA.	
XX			
AC	ABP59195;		
XX			
DT	01-MAY-2003	(first entry)	
XX			
DE	Human acetyl-Coenzyme A-carboxylase-alpha.		
XX			
KW	Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;		
KW	breast; ovary.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2002100896-A2.		
XX			
PD	19-DEC-2002.		
XX			
PF	12-JUN-2002; 2002WO-FR002015.		
XX			
PR	13-JUN-2001; 2001FR-00007740.		
PR	05-MAR-2002; 2002FR-00002788.		
XX			
PA	(CNRS ) CNRS CENT NAT RECH SCI.		
PA	(UYLY-) UNIV LYON 1 BERNARD CLAUDE.		
XX			
PI	Dalla Venezia NL, Magnard CM, Lenoir GM, Sinilnikova-Erard O;		
XX			
DR	WPI; 2003-175165/17.		
DR	N-PSDB; ABZ79442.		
XX			
PT	In vitro diagnosis of cancer, particularly breast and ovarian cancer, or		
PT	susceptibility, comprises detecting alterations in the acetyl coenzyme A-		
PT	carboxylase alpha gene or protein expression.		
XX			
PS	Disclosure; Page 49-56; 56pp; French.		
XX			
CC	The present sequence is the protein sequence for human acetyl-Coenzyme A-		
CC	carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro		
CC	diagnosis of cancer (or of an increased risk of developing it), by		
CC	detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha		
CC	protein expression, relative to a control population. The method is		
CC	particularly used to diagnose cancer, especially of breast or ovary, or		
CC	for assessing the risk of developing such cancers		
CC	for assessing the risk of developing such cancers		
XX			
SQ	Sequence 2346 AA;		
Query Match 61.3%; Score 1781; DB 6; Length 2346;			
Best Local Similarity 63.6%; Pred. No. 5.2e-157;			
Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;			
Qy	22	ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED	81
Db	103	ASP-AEFVTRFGGNKVIEKVLIANNGIAAVKCMRSIRRSWSEYEMFRNERAIRFVVMVTPED	161
Qy	82	LKVNADYIRMADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES	141
Db	162	LKANAEYIKWADHYVPVPGGANNNNYANVELILDIAKRIPQAVWAGWGHASENPKLPPEL	221
Qy	142	LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSD---	QGFL 198
Db	222	LL--KNGIAFMGPPNQAMWALGDKIASSIVAQTAGITPLPWSGSLRVWDQENDFSKRIL	279
Qy	199	TVSDDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNVAVLG	258
Db	280	NVPQELYEKGYVKDVGGLKAAEKVGYPMIKASEGGGKGIRKVNADDPPNLFROVQA	339
Qy	259	EVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEAPVTIAPED	318
Db	340	EVPGSPIFVMRLAKQSRHLEVQILADQYGNALISLFGDCSVQRHOKIIEEAPATIATPA	399
Qy	319	ARESMKAAVRLAKLVGYVSAGTVWELVSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP	378
Db	400	VFEHMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLQVEPCTEMVADVNL	458
Qy	379	AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSPSPESFKTKRQKPQGHVACRIT	438
Db	459	AAQLQIAMGIPLYRIKDIRMYGVSPWGSPIDFENSA-----HVP CPRGHVIAARIT	511
Qy	439	AENPDTGFKPCMGALTELNFRSSSTSTWGYFSVGTSGALHEYADSQGHIFAYGADRSEAR	498
Db	512	SENPDGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFAGSQGHCFSGWGENREEAI	571



QY	199	TVSDDVYQACIHTABEGLEKAEKIGYPMIKASEGGGKIRKCTNGEEFKQLYNAVLG	258
Db	280	NVPQELYEKGYKDVDDGLKAAEKVGYPMIKASEGGGKIRKVNADDFFNLFRQVQA	339
QY	259	EVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIIIEAPVTIAPED	318
Db	340	EVPGSPIFVMRLAKQSRHLEVQILADQYGNALISLFGRDCSVQRRHQKIIIEAPATIATPA	399
QY	319	AREMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPHTEMVSGVNIP	378
Db	400	VFEHMEQCAVKLAKMVGYSAGTVEYLYS-QDGSFYFLELNPRLQVEQPCTEMVADVNL	458
QY	379	AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTORKPQPGHVVACRIT	438
Db	459	AAQLQIAMGIPLYRIKDIRMYGVSPWGDSPIDFENSA-----HVPGRGHVIAARIT	511
QY	439	AENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR	498
Db	512	SENPDGFKPSSGTVOELNFRSNKNVWGYFSVAAAGGLHEFAGSQFGHCFPSWGENREEAI	571
QY	499	KQMVLSLKELSIRGDFRTTVEYLIKLETDAFESNKITTGWLDGLIQDRLTAERPPADLA	558
Db	572	SNMVVALKELSIRGDFRTTVEYLIKLETESQMNRI DTGWLDRLIAEKVRAERPDTMLG	631
QY	559	V 559	
Db	632	V 632	

**RESULT 20**

ABP59198  
ID ABP59198 standard; protein; 2346 AA.

AC ABP59198;

DT 01-MAY-2003 (first entry)

DE Human acetyl-Coenzyme A-carboxylase-alpha variant #2.

Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer; breast; ovary.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

```

FT Misc-difference 2271
FT /note= "Ala substituted with Val"

```

PN WO2002100896-A2.

PD 19-DEC-2002.

PF 12-JUN-2002; 2002WO-FR002015.

PR 13-JUN-2001; 2001FR-00007740.

PR 05-MAR-2002; 2002FR-00002788.

PA (CNRS) CNRS CENT NAT RECH SCI.

PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.

PI Dalla Venezia NL, Magnard CM, Lenoir GM, Sinilnikova-Erard O;

DR WPI; 2003-175165/17.

In vitro diagnosis of cancer, particularly breast and ovarian cancer, or PT susceptibility, comprises detecting alterations in the acetyl coenzyme A- PT carboxylase alpha gene or protein expression. PT

PS Example 2; Page; 56pp; French.

The present sequence is a variant sequence for human acetyl-Coenzyme A-carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro

diagnosis of cancer (or of an increased risk of developing it), by detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha protein expression, relative to a control population. The method is particularly used to diagnose cancer, especially of breast or ovary, or for assessing the risk of developing such cancers. Note: The present sequence was not shown in the specification, but was derived from information given

Sequence 2346 AA;

Query Match 61.3%; Score 1781; DB 6; Length 2346;  
Best Local Similarity 63.6%; Pred. No. 5.2e-157;  
Matches 344; Conservative 79; Mismatches 104; Indels 14

QY	22	ASPVADPIRKQGGHSHVITKVLICNNGIAAAYKEIRSIRKWAYETFGDERAIEFTVMATPED	81
Db	103	ASP-AEFVTRFGNKKVIEKVLIANNGIAAAYKCMRSIRRSYEMFRNERAIRFVVMVTPED	161
QY	82	LKVNADYIRMADQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES	141
Db	162	LKANAAYIKMADHYVPVPGANNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL	221
QY	142	LAASKHKIIFIGPGSAMRSLGDKISSTIVAQHADVPVCMPSWGTGIGKETMMSD--QGFL	198
Db	222	LL--XNGIAFMGPPNQAMWALGDKIASSIVAQTAGIPTLPWSGGLRVDWQENDFSKRIL	279
QY	199	TVSDDVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLG	258
Db	280	NVPQELYEKGVKVDVDDGLKAAEKVGPVMIKASEGGGKGIRKVNADDFPNLFQVQA	339
QY	259	EVPGSPVFMKLAQARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEAPVTIAPED	318
Db	340	EVPGSPIFVNLAKQSRHLEVQILADQYGNASIFGRDCSVQRRHQKIIIEAPATIATPA	399
QY	319	ARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEPAFLELNPRLQVEHPPTTEMVSGVNIP	378
Db	400	VFEHMEQCAVKLAKVGVVSAGTVEYLYS-QDGSFYFLELNPRLQVEQPCTEMVADVNL	458
QY	379	AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQRKPQPGHVWACRIT	438
Db	459	AAQLQIAMGIPLYRIKDIRMYGVSPWGDSPIDFENSA-----HVPCPRGHVIAARIT	511
QY	439	AENPDGPKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQGHIFAYGADRSEAR	498
Db	512	SENPDGPKPSSGTVQELNFRSNKNVWGYFSVAAAGLHEFAGSQFGHCFSWGNEREEAI	571
QY	499	KQMVLSKELSIIRGDFRTTVEYLIKLETDAFESNKITTCWLDGLIQDRLTAERPPADLA	558
Db	572	SNMVVALKELSIIRGDFRTTVEYLIKLETESFQMNRIIDTCWLDRLIAEKVRAERPDTMLG	631

## RESULT 21

ABB59490

ID ABB59490 standard; protein; 2348 AA.

AC ABB59490;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 5262.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS *Drosophila melanogaster*.

AA  
PN  
WO200171042-A2.

AX 27-SEP-2001.

PA 1007-225-17

XX PF 23-MAR-2001; 2001WO-US009231.  
XX PR 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX DR WPI; 2001-656860/75.  
XX DR N-PSDB; ABL03593.  
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX PS Disclosure; SEQ ID NO 5262; 2lpp + Sequence Listing; English.  
XX CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 2348 AA;  
Query Match 61.2%; Score 1780; DB 4; Length 2348;  
Best Local Similarity 64.2%; Pred. No. 6.5e-157;  
Matches 342; Conservative 69; Mismatches 110; Indels 12; Gaps 4;  
QY 27 DFIRKQGGHSHVITKVLICNNGIAA VKEIRSKWAYETFGDERAIEFTVMATPEDLKVNA 86  
Db 115 EFVKRFGGTRVINKVLIANNNGIAA VKCMRSIRRWAYEMFKNERAIRFVVMVTPEDLKANA 174  
QY 87 DYIRMADQYVEVPVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASK 146  
Db 175 EYIKMADHYVPVPGSGNNNNYANVELIVDIALRTQVAVWAGWGHASENPKLPELL--HK 232  
QY 147 HKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWPGTGIGIKETMMSDQGLTVSDDVYQ 206  
Db 233 EGLVFLGPPERAMWALGDKVASSIVAQTAEIPTLPWSGSDLKAQYSGKK--IKISSELF 290  
QY 207 QACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVF 266  
Db 291 RGCVTNVEOGLAAVNVKIGFPVMIKASEGGGKGIRRVDTTTEFPGLFRQVQAEVPGSPIF 350  
QY 267 VMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESM 326  
Db 351 VMKLARGARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVAIQAEVPEFMEKA 410  
QY 327 AVRLAKLVGYVSAGTVWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIIPAAQLQVAM 386  
Db 411 AVRLAKLVGYVSAGTVWLYDPE--GRYFFLELNPRLOVEHPCTEMVADVNLPAALQIQIGM 469  
QY 387 GIPLYSIRDITRLYGMDFRGNEVIDFDFSSPESFKTQKPOQGHVACRITAENPDTGF 446  
Db 470 GIPLYRLKDIRLLYGESPWGSSVIDFE-----NPPNKRPSGHVIAARITSENPDGEF 522  
QY 447 KPGMGALTENFRSSTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEARKQMVISLK 506  
Db 523 KPSSGTQVELNFRSKNVWGYFSAASGGLHEFADSFQGHCFWSGENRQQAENLVIALK 582  
QY 507 ELSIRGDFRTTVEYLIKLLETDAFESNKITTTGDLGLIQDRLTAERPDLAV 559  
Db 583 ELSIRGDFRTTVEYLIKLLETDNRFLDNSIDTAWLDALIAERVQSEKPDILLGV 635

RESULT 22  
AAO19075  
ID AAO19075 standard; protein; 2348 AA.  
XX AC AAO19075;  
XX DT 14-NOV-2002 (first entry)  
XX DE Drosophila melanogaster Acetyl-CoA carboxylase.  
XX KW Acetyl CoA carboxylase; enzyme; ACCase; insect; fruit fly; insecticide;  
XX KW acaricide.  
XX OS Drosophila melanogaster.  
XX PN DE10062422-A1.  
XX PD 20-JUN-2002.  
XX PF 14-DEC-2000; 2000DE-01062422.  
XX PR 14-DEC-2000; 2000DE-01062422.  
XX PA (FARB ) BAYER AG.  
XX PI Fischer R, Franken E, Nauen R, Teuschel U;  
XX DR WPI; 2002-644775/70.  
XX DR N-PSDB; AAL49486.  
XX PT New nucleic acid encoding insect acetyl-coenzyme A carboxylase, useful  
PT for identifying insecticidal and acaricidal agents, also related proteins  
PT and modulators.  
XX PS Claim 8; Page 21-28; 34pp; German.  
XX CC The present invention provides the protein and coding sequences of the  
CC Drosophila melanogaster acetyl CoA carboxylase enzyme (ACCase). The  
CC sequences can be used to identify insecticidal and acaricidal agents that  
CC act by modulating activity or expression of ACCase. The present sequence  
CC is the protein of the invention  
XX SQ Sequence 2348 AA;  
Query Match 61.2%; Score 1780; DB 5; Length 2348;  
Best Local Similarity 64.2%; Pred. No. 6.5e-157;  
Matches 342; Conservative 69; Mismatches 110; Indels 12; Gaps 4;  
QY 27 DFIRKQGGHSHVITKVLICNNGIAA VKEIRSKWAYETFGDERAIEFTVMATPEDLKVNA 86  
Db 115 EFVKRFGGTRVINKVLIANNNGIAA VKCMRSIRRWAYEMFKNERAIRFVVMVTPEDLKANA 174  
QY 87 DYIRMADQYVEVPVPGSGNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASK 146  
Db 175 EYIKMADHYVPVPGSGNNNNYANVELIVDIALRTQVAVWAGWGHASENPKLPELL--HK 232  
QY 147 HKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWPGTGIGIKETMMSDQGLTVSDDVYQ 206  
Db 233 EGLVFLGPPERAMWALGDKVASSIVAQTAEIPTLPWSGSDLKAQYSGKK--IKISSELF 290  
QY 207 QACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVF 266  
Db 291 RGCVTNVEOGLAAVNVKIGFPVMIKASEGGGKGIRRVDTTTEFPGLFRQVQAEVPGSPIF 350  
QY 267 VMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESM 326  
Db 351 VMKLARGARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEEAPVAIQAEVPEFMEKA 410  
QY 327 AVRLAKLVGYVSAGTVWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIIPAAQLQVAM 386  
Db 411 AVRLAKLVGYVSAGTVWLYDPE--GRYFFLELNPRLOVEHPCTEMVADVNLPAALQIQIGM 469  
QY 387 GIPLYSIRDITRLYGMDFRGNEVIDFDFSSPESFKTQKPOQGHVACRITAENPDTGF 446

Db 470 GIPLYRLKDIRLLYGESPWSSVIDFE-----NPPNKPSPGHVIAARITSENPDGEF 522  
QY 447 KPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFHIFAYGADRSEARKQMVISLK 506  
Db 523 KPSSGTVQELNFRSSKNVWGYFSVAASGGLHEFADSQFHCFSGWENRQQAENLVIALK 582  
QY 507 ELSIRGDFRTTVEYLKLETDAFESNKITTTGWLDDGLIQDRLTAERPPADLAV 559  
Db 583 ELSIRGDFRTTVEYLITLLETNRFLDNSIDTAWLDALIAERVOSEKPDILLGV 635  
RESULT 23  
ABB83866  
ID ABB83866 standard; protein; 2348 AA.  
XX  
AC ABB83866;  
XX  
DT 04-OCT-2002 (first entry)  
XX  
DE Drosophila melanogaster ACCase SEQ ID NO 2.  
XX  
KW Drosophila melanogaster; fruit fly; Acetyl-CoA carboxylase; ACCase;  
KW insecticide; acaricide; EC 6.4.1.2; enzyme.  
XX  
OS Drosophila melanogaster.  
XX  
PN DE10062421-A1.  
XX  
PD 20-JUN-2002.  
XX  
PF 14-DEC-2000; 2000DE-01062421.  
XX  
PR 14-DEC-2000; 2000DE-01062421.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Franken E, Nauen R, Teuschel U;  
XX  
DR WPI; 2002-584630/63.  
XX N-PSDB; ABB85738.  
XX  
PT New nucleic acid encoding insect acetyl-coenzyme A carboxylase, useful  
PT for identifying insecticidal and acaricidal agents, also related proteins  
PT and modulators.  
XX  
PS Claim 8; Page 21-27; 34pp; German.  
XX  
CC The invention relates to a novel nucleic acid (I) comprising (i) a 4047  
CC bp sequence (ABN85738) or AAF59156; (ii) a segment with at least 14 bp  
CC from (i); (iii) a sequence that hybridizes to (i) or (ii) at 37-50oC;  
CC (iv) a sequence at least 60% identical with (i) or (ii); (v) a complement  
CC of (i)-(iv) or (vi) an equivalent of (i)-(iv) within the degeneracy of  
CC the genetic code. (I) and the encoded polypeptide (II, ABB83866) having  
CC ACCase (acetyl-CoA carboxylase, EC 6.4.1.2) activity are used to identify  
CC insecticidal and acaricidal agents that act by modulating activity or  
CC expression of ACCase, an essential enzyme for survival of insects. The  
CC present sequence is that of the Drosophila melanogaster ACCase of the  
CC invention  
XX  
SQ Sequence 2348 AA;

Query Match 61.2%; Score 1780; DB 5; Length 2348;  
Best Local Similarity 64.2%; Pred. No. 6.5e-157;  
Matches 342; Conservative 69; Mismatches 110; Indels 12; Gaps 4;  
QY 27 DFIRKQGGHVSITKVLICNNGIAAIVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNA 86  
Db 115 EFVKRFGGTRVINKVLIANNGIAAIVKCMRSIRRWAYEMFKNERAIRFVVMVTPEDLKANA 174  
QY 87 DYIRMADQYVEVPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPESLAASK 146  
Db 175 EYIKMADHYVPVPGGSNNNNYANVELIVDIALRTQVQAVWAGWGHASENPKLPPELL--HK 232

QY 147 HKIIFIGPPGSAMRSLGDKISSTIVAQAHADVPCMPWSGTGKETMMSDQGLFTVSDDDVYQ 206  
Db 233 EGLVFLGPPERAMWALGDKVASSIVAQTAEIPTLPWSGDLKAQYSGKK--IKISSELF 290  
QY 207 QACIHTAEGLEKAEKIGYPMIKASEGGGGKGIKCTNGEEFKQLYNVLGEVPGSPVF 266  
Db 291 RGCVTNVEQGLAAVNKIGFPMIKASEGGGGKGIKCTNGEEFKQLYNVLGEVPGSPVF 350  
QY 267 VMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEAPVTIAPEDAREMEKA 326  
Db 351 VMKLAGARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEAPVTIAPEDAREMEKA 410  
QY 327 AVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVINIPAAQLQVAM 386  
Db 411 AVRLAKMVGYVSAGTVEWLYDPE-GRYFFLELNPRLOVEHPTTEMVADVNLPAALQIGM 469  
QY 387 GIPLYSIDRTLYGMDPRGNEVIDFDFFSSPESFKTQKQPQGHVACRITAENPDITGF 446  
Db 470 GIPLYRLKDIRLLYGESPWSSVIDFE-----NPPNKPSPGHVIAARITSENPDGEF 522  
QY 447 KPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFHIFAYGADRSEARKQMVISLK 506  
Db 523 KPSSGTVQELNFRSSKNVWGYFSVAASGGLHEFADSQFHCFSGWENRQQAENLVIALK 582  
QY 507 ELSIRGDFRTTVEYLKLETDAFESNKITTTGWLDDGLIQDRLTAERPPADLAV 559  
Db 583 ELSIRGDFRTTVEYLITLLETNRFLDNSIDTAWLDALIAERVOSEKPDILLGV 635

RESULT 24

ABB86033  
ID AAB86033 standard; protein; 2288 AA.  
XX  
AC AAB86033;  
XX  
DT 13-JUL-2001 (first entry)  
XX  
DE Bovine acetyl-coenzyme A carboxylase-alpha protein fragment.  
XX  
KW Acetyl-coenzyme A carboxylase-alpha; acetyl-coA carboxylase alpha;  
KW bovine; milk gland-specific promoter; Accalpha; milk production; sheep;  
KW goat; fat content; genotyping; lactation.  
XX  
OS Bos taurus.  
XX  
PN DE19946173-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 20-SEP-1999; 99DE-01046173.  
XX  
PR 20-SEP-1999; 99DE-01046173.  
XX  
PA (BIOL-) FORSCHUNGSINSTITUT BIOLOGIE LANDWIRTSCHA.  
XX  
PI Seyfert HM;  
XX  
DR WPI; 2001-258968/27.  
DR N-PSDB; AAF88002.  
XX  
PT New nucleic acid encoding bovine acetyl coenzyme A carboxylase alpha and  
PT its promoter, for milk-specific production of proteins and for regulating  
PT fat content of milk.  
XX  
PS Claim 2c; Page 24-30; 44pp; German.  
XX  
CC This invention describes a novel milk gland-specific promoter of the  
CC bovine acetyl coenzyme A carboxylase alpha gene (Accalpha), or its  
CC fragments, which are used to control expression of foreign genes. When  
CC the promoter (or the Accalpha structural gene) is replaced, at least in  
CC part, by a sequence that is altered by deletion or substitution, then  
CC expression of Accalpha in the milk gland is reduced and the milk produced



CC (by cattle, sheep or goats) has reduced fat content. Analysis of the  
CC polymorphic 933-966 region of (Accalpha) is useful for genotyping  
CC animals, producing a genotype that is directly correlated with Accalpha  
CC expression during lactation and with fat content of the milk. This makes  
CC it possible to generate populations of cattle that produce milk of high  
CC or low fat content by classical breeding methods. Accalpha is a lactation  
CC -specific, inducible promoter for expressing foreign proteins in the milk  
CC and, when modified, results in milk of reduced fat content, which  
CC facilitates recovery of proteins. This sequence represents a fragment  
CC from bovine Accalpha which contains a fragment of exon 5A exon 6 and exon  
CC 7  
XX  
SQ

Sequence 2288 AA;

Query Match 61.1%; Score 1775; DB 4; Length 2288;  
Best Local Similarity 63.7%; Pred. No. 1.8e-156;  
Matches 345; Conservative 78; Mismatches 103; Indels 16; Gaps 6;

QY 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED 81  
DB 45 ASP-AEFVTRFGGNRVIEKVLIANNGIAAIVKESIRRSYEMFRNERAIRFVVMVTPED 103  
QY 82 LKVNADYIRMDQYVEVPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141  
DB 104 LKANAEYIKMADHYVPVPGGPNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL 163  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAHQADVPCMPWSGTGI----KETMMSDQGF 197  
DB 164 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSLCVDWHENDFSKR-I 220  
QY 198 LTVSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEETFQKLYNAVL 257  
DB 221 LNVPOELYEKGYVKDDVDDGLKAAEEVGPVMIKASEGGGKGIKRVNNADDFPNLFRQVQ 280  
QY 258 GEVFGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAPE 317  
DB 281 AEVPGSPIFVMRLAKQSRHLEVQILADQYGNALISLFGDCSVQRRHQKIEEAPAAIATP 340  
QY 318 DARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNI 377  
DB 341 AVFHEMQCAVKLARMGVYVSAGTVEYLYS-QDGSFYFLELNPRLOVEHPCTEMVADVNL 399  
QY 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTKRQKPOQGHVACRI 437  
DB 400 PAAQLQIAMGIPLYRIKDIRMMYGVSPWGDAPIDFENSA-----HVPCPRGHVIAARI 452  
QY 438 TAENPDGTGFKPGMGALTENLFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA 497  
DB 453 TSENPDGFKPSSGTVOELNFRSNKNVWGYFSAAGGLHEFADSQFGHCFSWGENREEA 512  
QY 498 RKQMVLSKELSIKRGDFRTTVEYLIKLETDAFESNKITTTGLDGLIQDRLTAERPPADL 557  
DB 513 ISNMVVALKELSIKRGDFRTTVEYLIKLETTESFQNLNRIKGTGLDRLIAEKVQAEPRDTML 572  
QY 558 AV 559  
DB 573 GV 574

RESULT 25

AAR05707

ID AAR05707 standard; protein; 2324 AA.

XX

AC AAR05707;

DT 25-MAR-2003 (revised)

DT 16-AUG-1990 (first entry)

XX

DE Acetyl-CoA-carboxylase.

XX

KW Acetyl-CoA-carboxylase; Co2 ligase; malonyl-CoA; biotin;

KW Biotin:carboxylase; carboxyl-transferase; acetyl-CoA; ATP; ds.

XX

OS Gallus sp.

XX

PN JP02057179-A.

XX

PD 26-FEB-1990.

XX

PF 24-AUG-1988; 88JP-00208170.

XX

PR 24-AUG-1988; 88JP-00208170.

XX

PA (MEIP ) MEIJI MILK PROD CO LTD.

XX

DR WPI; 1990-104915/14.

DR N-PSDB; AAQ04013.

XX

PT Acetyl-coa-carboxylase - derived from chicken liver, has known nucleotide

PT and amino acid sequence.

XX

PS Disclosure; Fig 2; 14pp; Japanese.

XX

CC Gene derived from chicken liver. (Updated on 25-MAR-2003 to correct PA

CC field.)

XX

SQ Sequence 2324 AA;

Query Match 61.0%; Score 1774; DB 2; Length 2324;

Best Local Similarity 63.0%; Pred. No. 2.3e-156;

Matches 341; Conservative 83; Mismatches 103; Indels 14; Gaps 5;

QY 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED 81  
DB 103 ASP-AEFVTRFGGNRVIEKVLIANNGIAAIVKESIRRSYEMFRNERAIRFVVMVTPED 161  
QY 82 LKVNADYIRMDQYVEVPGGSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141  
DB 162 LKANAEYIKMADHYVPVPGGPNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL 221  
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAHQADVPCMPWSGTGKETMMSD---QGFL 198  
DB 222 L--HKNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWNSGLRVWDQENDLQKRIL 279  
QY 199 TVSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEETFQKLYNAVLG 258  
DB 280 NVPQELYEKGYVKDADDGLRAAEVGPVMIKASEGGGKGIKRVNNADDFPNLFRQVQA 339  
QY 259 EVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAPED 318  
DB 340 QVPGSPIFVMRLAKQSRHLEVQILADQYGNALISLFGDCSVQRRHQKIEEAPASIATSV 399  
QY 319 ARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP 378  
DB 400 VFEHMEQCAVKLARMGVYVSAGTVEYLYS-QDGSFYFLELNPRLOVEHPCTEMVADVNL 458  
QY 379 AAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTKRQKPOQGHVACRIT 438  
DB 459 AAQLQIAMGIPLYRIKDIRMMYGVSPWGDGSDIFENSA-----HVPCPRGHVIAARIT 511  
QY 439 AENPDGTGFKPGMGALTENLFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498  
DB 512 SQNPDEGFKPSSGTVOELNFRSNKNVWGYFSAAGGLHEFADSQFGHCFSWGENREEAI 571  
QY 499 KQMVLSKELSIKRGDFRTTVEYLIKLETDAFESNKITTTGLDGLIQDRLTAERPPADLA 558  
DB 572 SNMVVALKELSIKRGDFRTTVEYLIKLETTESFQNLNRIKGTGLDRLIAEKVQAEPRDTMLG 631  
QY 559 V 559  
DB 632 V 632

RESULT 26

ABM83569

ID ABM83569 standard; protein; 2420 AA.







CC (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis,  
CC etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris,  
CC hypertension, Raynaud's disease, myocarditis, pericarditis, etc;  
CC neurological disorders e.g. epilepsy, Huntington's disease, Parkinson's  
CC disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and  
CC developmental disorders e.g. Duchenne and Becker muscular dystrophy,  
CC cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of  
CC the invention can also be used for drug screening, proteome analysis,  
CC microarrays creating knock-in humanised animals or transgenic animals to  
CC model human diseases, in somatic or germline gene therapy, to generate a  
CC transcript image of a tissue or cell type, for detecting differences in  
CC the chromosomal location due to translocation, inversion, etc., among  
CC normal, carrier or affected individuals, and as hybridization probes for  
CC mapping naturally occurring genomic sequences. ABB84649-ABB84673  
CC represent secreted proteins encoded by the cDNA's shown in ABS57545-  
CC ABS57569, described in the disclosure of the invention  
XX  
SQ Sequence 2487 AA;

Query Match 60.9%; Score 1769.5; DB 6; Length 2487;  
Best Local Similarity 63.4%; Pred. No. 6.9e-156;  
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;

Qy 22 ASPVADFIRKQGGHSHVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81  
Db 245 ASP-AEEFTRFGGDRVIEKVLIANNGIAAVKMRISRRWAYEMFRNERAIRFVVMVTPED 303  
Qy 82 LKVNADYIRMADQYVEVPGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141  
Db 304 LKANAEXIKVADHYVPVPGGPNNNYANVELIVDAKRIPVQAVWAGWGHASENPKLP 363  
Qy 142 LAASKHKIIFIPGPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGKETMMSD---QG-F 197  
Db 364 LC--KNGVAFLGPPSEAMWALGDKIASTVVAQTLPVTPWSSGLTVEWTEDDLQOQKR 421  
Qy 198 LTVSDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVL 257  
Db 422 ISVPEDVYDKGVKDVDEGLEAAERIGFPLMIKASEGGGKGIRKAESAEDFPILFRQVQ 481  
Qy 258 GEVPGSPVFMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRRHQKIIIEEAPVTIAPE 317  
Db 482 SEIPGSPIFLMKLAQHARHLEVQILADQYGNASVLFGRDCSIQRRHQKIVEEAPATIAPL 541  
Qy 318 DARESMKAAVRLAKLVGYVSAGTVVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377  
Db 542 AIFEFMEQCAIRLAKTVGYVSAGTVVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL 600  
Qy 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSPSPESFKT-ORKPQPQGHVVACR 436  
Db 601 PAAQLQIAMGVPLHRLKDIRLLYGESPWG-----VTPISFETPSNPPLARGHVIAR 652  
Qy 437 ITAENPDTGFKPGMGALTENLFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE 496  
Db 653 ITSENPDGFKPSSGTQVELNFRSSKNVWGYFSAATGGLHEFADSQFGHCFESNGENREE 712  
Qy 497 ARKQMVISLKELSIKRGDRTTVEYLYKLLETDAFESKNITTGWLDGLIQDRLTAERPPAD 556  
Db 713 AISNMVVALKELSIKRGDRTTVEYLYLINLLETESFQNDIDTGWLDYLIAEKVQAEKPDIM 772  
Qy 557 LAV 559  
Db 773 LGV 775

RESULT 29  
ABU65149  
ID ABU65149 standard; protein; 2498 AA.  
XX  
AC ABU65149;  
XX  
DT 20-MAY-2003 (first entry)  
XX

DE Human NOV76a protein.  
XX  
KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;  
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;  
KW human.  
XX  
OS Homo sapiens.  
PN WO200272757-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 08-MAR-2002; 2002WO-US006908.  
PR 08-MAR-2001; 2001US-0274101P.  
PR 08-MAR-2001; 2001US-0274194P.  
PR 08-MAR-2001; 2001US-0274281P.  
PR 08-MAR-2001; 2001US-0274322P.  
PR 09-MAR-2001; 2001US-0274849P.  
PR 12-MAR-2001; 2001US-0275235P.  
PR 13-MAR-2001; 2001US-0275578P.  
PR 13-MAR-2001; 2001US-0275579P.  
PR 13-MAR-2001; 2001US-0275601P.  
PR 14-MAR-2001; 2001US-0276000P.  
PR 16-MAR-2001; 2001US-0276776P.  
PR 19-MAR-2001; 2001US-0276994P.  
PR 20-MAR-2001; 2001US-0277239P.  
PR 20-MAR-2001; 2001US-0277321P.  
PR 20-MAR-2001; 2001US-0277327P.  
PR 21-MAR-2001; 2001US-0277791P.  
PR 22-MAR-2001; 2001US-0277833P.  
PR 23-MAR-2001; 2001US-0278152P.  
PR 26-MAR-2001; 2001US-0278894P.  
PR 27-MAR-2001; 2001US-0278999P.  
PR 27-MAR-2001; 2001US-0279036P.  
PR 28-MAR-2001; 2001US-0279344P.  
PR 30-MAR-2001; 2001US-0277338P.  
PR 30-MAR-2001; 2001US-0279995P.  
PR 30-MAR-2001; 2001US-0280233P.  
PR 02-APR-2001; 2001US-0280802P.  
PR 02-APR-2001; 2001US-0280822P.  
PR 02-APR-2001; 2001US-0280900P.  
PR 04-APR-2001; 2001US-0281194P.  
PR 13-APR-2001; 2001US-0283675P.  
PR 30-APR-2001; 2001US-0287424P.  
PR 02-MAY-2001; 2001US-0288066P.  
PR 03-MAY-2001; 2001US-0288342P.  
PR 03-MAY-2001; 2001US-0288528P.  
PR 15-MAY-2001; 2001US-0291190P.  
PR 16-MAY-2001; 2001US-0291099P.  
PR 16-MAY-2001; 2001US-0291240P.  
PR 30-MAY-2001; 2001US-0294485P.  
PR 31-MAY-2001; 2001US-0294889P.  
PR 31-MAY-2001; 2001US-0294899P.  
PR 18-JUN-2001; 2001US-0299027P.  
PR 19-JUN-2001; 2001US-0299303P.  
PR 19-JUN-2001; 2001US-0299310P.  
PR 10-JUL-2001; 2001US-0304354P.  
PR 31-JUL-2001; 2001US-0309198P.  
PR 16-AUG-2001; 2001US-0312903P.  
PR 10-SEP-2001; 2001US-0318462P.  
PR 12-SEP-2001; 2001US-0318770P.  
PR 27-SEP-2001; 2001US-0325430P.  
PR 27-SEP-2001; 2001US-0325681P.  
PR 18-OCT-2001; 2001US-0330380P.  
PR 31-OCT-2001; 2001US-0335301P.  
PR 14-NOV-2001; 2001US-0332172P.  
PR 14-NOV-2001; 2001US-0332271P.  
PR 14-NOV-2001; 2001US-0332272P.  
PR 14-NOV-2001; 2001US-0333184P.  
PR 14-NOV-2001; 2001US-0333272P.  
PR 21-NOV-2001; 2001US-0332094P.  
PR 03-DEC-2001; 2001US-0337426P.









Query Match	58.4%;	Score 1697.5;	DB 8;	Length 2206;
Best Local Similarity	63.7%;	Pred. No. 3.4e-149;		
Matches 324;	Conservative 74;	Mismatches 98;	Indels 13;	Gaps 4;
QY	54	IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIIRMADQYVEVPGSSNNNNYANVDLI	113	
Db	1	MRSIRRSWSEMFERNERAIRFVVMVTPEDLKANAIEYIKMADHYVPVPGPNNNNYANVELI	60	
QY	114	VDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQ	173	
Db	61	LDIAKRIPVQAVWAGWGHASENPKLPDLL--KNGIAFMGPPSQAMWALGDKIASSIVAQ	118	
QY	174	HADVPCMPWSGTGIKETMMSD---QGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIK	230	
Db	119	TAGIPTLPWSGSLRVWDQWENDESKRILNVPELYEKGYKVDVDDGLQAAEEVGYPMIK	178	
QY	231	ASEGGGKGIRKCTNGEEFKQLYNAVLEVPGSPVFMKLAGQARHLEVLQLLADQYGNAI	290	
Db	179	ASEGGGKGIRKVNADDFPNLFRQVQAEVPGSPIFVFMRLAKQSRHLEVLQILLADQYGNAI	238	
QY	291	SIFGRDCSVQRRHQKIIIEEAPVTIAPEDARESMEEKAAVRLAKLVGYVSAGTVEWLYSPES	350	
Db	239	SIFGRDCSVQRRHQKIIIEEAPATIATPAVFEHMEQCAVKLAKWGYVSAGTVEYLYS-QD	297	
QY	351	GEFAPLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVI	410	
Db	298	GSFYFLELNPRLQVEHPCTEMVADVNLPAALQQLIAMGIPLYRIKDIRMYGVSPWGDSP	357	
QY	411	DFDFSSPESFKTQKQPQGHVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSV	470	
Db	358	DFEDSA-----HVPCPRGHVIAARITSENPDDEGFKPSSGTVQELNFRSNKNVWGYFSV	410	
QY	471	GTSGALHEYADSOFGHIFAYGADRSEARKQMVISLKELSRGDFRTTVEYLYLKLETDAP	530	
Db	411	AAAGGLHEIADSOFGHCFSGWGENREEAISNMVVALKELSRGDFRTTVEYLYLKLETESF	470	
QY	531	ESNKITTGWLGLDGLIQRDLTAERPPADLAV	559	
Db	471	QMNRIDTGWLDRLIAEKVQAEPRDPTMLGV	499	
RESULT 33				
ADQ90746				
ID	ADQ90746	standard; protein; 2483 AA.		
XX	AC	ADQ90746;		
XX	XX	21-OCT-2004 (first entry)		
DE	Human acetyl-coenzyme A carboxylase - ACC2.			
KW	human; carboxyltransferase domain; CT domain;			
KW	acetyl-coenzyme A carboxylase; acetyl-CoA carboxylase;			
KW	metabolic syndrome; diabetes; obesity; cardiovascular disease;			
KW	atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia;			
KW	hypertension; hyperuricaemia; renal dysfunction;			
KW	crystallisable composition; enzyme; ACC2.			
OS	Homo sapiens.			
XX	WO2004063715-A2.			
PN	29-JUL-2004.			
XX	09-JAN-2004; 2004WO-US0000585.			
XX	10-JAN-2003; 2003US-0439383P.			
PR	31-MAR-2003; 2003US-0459464P.			
PR	31-JUL-2003; 2003US-0491640P.			
PR	27-OCT-2003; 2003US-0514636P.			
PR	09-JAN-2004; 2004US-00514636.			
XX	XX			

PA	(UYCO ) UNIV COLUMBIA NEW YORK.		
XX			
PI	Tong L, Zhang H, Yang Z;		
XX			
DR	WPI; 2004-571486/55.		
XX			
PT	New crystallizable composition comprising a carboxyltransferase domain of		
PT	acetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes, obesity,		
PT	cardiovascular disease, atherosclerosis, or cancer.		
XX			
PS	Example 4; SEQ ID NO 9; 195pp; English.		
XX			
CC	The invention comprises a crystallisable composition containing a		
CC	carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA)		
CC	carboxylase. The composition of the invention is useful for treating:		
CC	metabolic syndrome, diabetes, obesity, cardiovascular disease,		
CC	atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia,		
CC	hypertension, hyperuricaemia and renal dysfunction. The present amino		
CC	acid sequence represents a human acetyl-CoA carboxylase of the invention.		
XX			
SQ	Sequence 2483 AA;		
Query Match		57.4%;	
Best Local Similarity		60.8%;	
Matches 330;		Conservative 79;	
		Mismatches 117;	
		Indels 17;	
		Gaps 8;	
QY	22	ASPVADFIRKQGHSVITKVLICNNGIAAARKVIRKWAYETFGDERAIEFTVMATPED 81	
Db	244	ASP-AEFVTRFGDRVIEKVLIANNGIAAARKVIRKWAYETFGDERAIEFTVMATPED 302	
QY	82	LKNADYIIRMADQYVEVPGSSNNNNYANVDLIVDAERAGVHAVWAGWGHASENPRLPES 141	
Db	303	LKANAIEYIKMADHYGPAFGGPNNNNYANVELIVDAERAGVHAVWAGWGHASENPKLP 362	
QY	142	LAASKHKIIFIGPPG-SAMRSLGDKISSTIVAQHADVPMPWSGTGIKETMMSD---QG- 196	
Db	363	LC--KNGVAFGLPRLRPMVGLGDKIASTVVAQTLOVPTLPRSGSALTVEWTEDDLQOGK 420	
QY	197	FLTVSDDVYQQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNV 256	
Db	421	RISVPEDVYDKGVKVDDEGLEAAERIGFPLMIKASEGGGKGIRETESAEDPILFRQV 480	
QY	257	LGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAP 316	
Db	481	QSEIPGSPIFLMKLAQHARHLEVQILLADQYGNALISIFGRDCSVQRRHQKIEEAPATIAP 540	
QY	317	EDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVN 376	
Db	541	LAIFEFEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHLELNPRLQVEHPCTEMIADV 599	
QY	377	IPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDEDFSSPESFKTQKQPQGHVVACR 436	
Db	600	LPAAQLQIAMGAPLHRLKDIRLLYGESPWGDSPISPENSA-----HLPCCRGHVIATR 652	
QY	437	ITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOFGHIFAYGADRSE 496	
Db	653	ITSENPDGFKPSSGTVQELNFRSSKNVWGYFTVAATGGLHEFAISQFGHCFSGWGENRKE 712	
QY	497	ARKQMVISLKELSRGDFRTTVEYLYLKLETDAPESNKITTGWLGLIQRDLTAERPPAD 556	
Db	713	AISNMVVALKELSLRGDFRTTVEYLYLNLETESFQNNYIDTGWLDYLIAEKV-QKKPNIM 771	
QY	557	LAV 559	
Db	772	LGV 774	
RESULT 34			
ADQ39507			
ID	ADQ39507	standard; protein; 2483 AA.	
XX	AC	ADQ39507;	
XX	XX		













Db 280 PPGSSLVTIPEEMYRQACVYTTTEEAVASQVVGYPAMIKASWGGGKGIRKVHDDDEVRA 339  
Qy 252 LYNALGVEVPGSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKIIIEAP 311  
Db 340 LFKQVQGEVPGSPIFIMKVASQSRHLEVQLLCDQYGNVSAHLSRDCSVQRRHQKIIIEGP 399  
Qy 312 VTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTEM 371  
Db 400 ITVAPRDTVKKLEQAARRLAKSVNYVGAATVEFLYSMDTGDFYFLELNPRLQVEHPVTER 459  
Qy 372 VSGVNIIPAAQLQVAMGIPLYISIRDIRTLTYGMDPRGNEVIDFDFSSPESFKTQKQPQGH 431  
Db 460 IADINLPAAQVAVGMGIPLWQIPEIRRFYGIEQYDSWRTTSLASPFNFDKAESVRPKGH 519  
Qy 432 VVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYG 491  
Db 520 CVAVRTSEDDGFKPTSGQVQELSPKSNPNVWGYFSVKSGGGIEHFSDSQFGHVFAPG 579  
Qy 492 ADRSEARKQMVISLKELSIRGDFRTTVEYLYIKLLETDAFESNKITTGWLDGLIQDRLTAE 551  
Db 580 ESRAMAIANMVLALKEIQIRGEVRTNVDTIDLLHAFDYRENKIHTGWLDSRIAMRVRAE 639  
Qy 552 RPPADLAV 559  
Db 640 RPPWYLSV 647

RESULT 40

ABB91251  
ID ABB91251 standard; protein; 2359 AA.

XX AC ABB91251;

DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 462.

XX KW Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

XX PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP009892.

XX PR 28-AUG-2001; 2001WO-EP009892.

XX PA (FARB ) BAYER AG.

XX PI Tietjen K, Weidler M;

XX DR WPI; 2002-269010/31.

XX PT Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
XX organisms.

PS Claim 5; SEQ ID NO 462; 261pp + Sequence Listing; English.

XX CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
XX herbicides

XX SQ Sequence 2359 AA;

Query Match 54.4%; Score 1581.5; DB 5; Length 2359;  
Best Local Similarity 53.3%; Pred. No. 3.3e-138;  
Matches 305; Conservative 95; Mismatches 137; Indels 35; Gaps 8;  
Qy 12 IGGNPLETAPASPA--DFIRKQGGHVSITKVLICNNGIAAATKESIRKWAYETFGDE 68  
Db 110 VNGYHSDVVPGRNVAEVEFCKALGGKRPISILVATNGMAAVKFIRSVRTWAYETFGSE 169  
Qy 69 RAIEFTVMATPEDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDVAERAGVHAWAG 128  
Db 170 KAVKLVAMATPEDMRINAEHRIADQFVEVPGSGTNNNNYANVQLIVEMAETVRDVAWPG 229  
Qy 129 WGHASENPRLPESLAASKHK-IIFIGPPGSAMESLGDKISSTIVAQAHADVPCMPWSGTGI 187  
Db 230 WGHASENPELPDAL---KEKGIIFLGPADSMIALGDKIGSSLIAQAADVTLFWSGSHV 286  
Qy 188 KETMMSDQGLTVSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGGKGIRKCTNGE 247  
Db 287 K-IPPGRSLVTVPPEIYKACVYTTTEEAIASQCVVGYPPAMIKASWGGGKGIRKVHND 344  
Qy 248 EFKQLYNAVLEVPSPVFMKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQRRHQKII 307  
Db 345 EVRALFKVQVQGEVPGSPIFIMKVASQSRHLEAQLLCDQYGNVAALHSRDCSVQRRHQKII 404  
Qy 308 EEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHP 367  
Db 405 EEPITVAPQETIKLEQAARRLAKSVNYVGAATVEYLYSMDTGYYFLELNPRLQVEHP 464  
Qy 368 TTEMVSGVNIIPAAQLQVAMGIPLYISIRDIRTLTYGMDPRG-----NEVI--DFDFSPE 418  
Db 465 VTEWIAEVLNLPAAQVAVGMGIPLWQIPEIRRFYGMHGGGYDSWRKTSVVASPFDFDEAE 524  
Qy 419 SPKTQKPOQGHVVACRITAENPDGTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHE 478  
Db 525 SLR-----PKGHCVAVRTSEDDGFKPTSGEIQLSFKSKPNMWSYFSVKSGGSIHE 578  
Qy 479 YADSQFG-----HIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLYIKLLET 527  
Db 579 FSDSQFGKLNKFKGMLGQHVFAFGESRSVAIANMVLALKEIQIRGDIRTNVDYTTIDLLHA 638  
Qy 528 DAFESNKITTGWLDGLIQDRLTAERPPADLAV 559  
Db 639 SDYRENKIHTGWLDSRIAMRVRAERPPWYLSV 670

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